



09573569 Sequence Listing.txt

SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANT: Maassab, Hunein F
Herlocher, Martha L
 - (ii) TITLE OF INVENTION: Cold-adapted Influenza Virus
 - (iii) NUMBER OF SEQUENCES: 40
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Anna M Lewak
 - (B) STREET: 5445 Corporate Drive
 - (C) CITY: Troy
 - (D) STATE: MI
 - (E) COUNTRY: USA
 - (F) ZIP: 48098
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US/08/573,569
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US/08/082,846
 - (B) FILING DATE:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lewak, Anna M
 - (B) REGISTRATION NUMBER: 33006
 - (C) REFERENCE/DOCKET NUMBER: 2115-00257
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 313-641-1600
 - (B) TELEFAX: 313-641-0270
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 890 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: RNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Influenza virus
 - (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: NS

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- (ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 27..56
 (D) OTHER INFORMATION: /product= "nonstructural protein NS2"
 /gene= "NS"
 /note= "nonstructural protein NS2"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: conflict
 (B) LOCATION: replace(483, "a")
 (D) OTHER INFORMATION: /note= "a in ca "master" strain and in wt2(3)"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 529..861
 (D) OTHER INFORMATION: /product= "nonstructural protein NS2"
 /gene= "NS"
 /note= "nonstructural protein NS2"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: conflict
 (B) LOCATION: replace(813, "g")
 (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3)"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: join(27..56, 529..861)
 (D) OTHER INFORMATION: /product= "nonstructural protein NS2"
 /gene= "NS"
 /note= "nonstructural protein NS2"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 27..677
 (D) OTHER INFORMATION: /product= "nonstructural protein NS1"
 /gene= "NS"
 /note= "nonstructural protein NS1"
 /citation= ([1][2])
- (x) PUBLICATION INFORMATION:
 (A) AUTHORS: Herlocher, M L
 Maassab, H F
 Webster, R G
 (B) TITLE: Molecular and biological changes in the cold
 adapted master strain A/AA/6/60 (H2N2) influenza
 virus
 (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
 (G) DATE: 1993
 (K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 890
- (x) PUBLICATION INFORMATION:
 (A) AUTHORS: Cox, N J

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Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain, A/Ann Arbor/6/60(H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCAAAAGCA GGGUGACAAA GACAU	AUG GAU CCU AAC ACU GUG UCA AGC UUU	53
	Met Asp Pro Asn Thr Val Ser Ser Phe	
	1 5	
CAG GUA GAU UGC UUC CUU UGG CAU GUC CGC AAA CAA GUU GCA GAC CAA		101
Gln Val Asp Cys Phe Leu Trp His Val Arg Lys Gln Val Ala Asp Gln		
10 15 20 25		
GAA CUA GGU GAU GCC CCA UUC CUU GAU CGG CUU CGC CGA GAU CAG AAG		149
Glu Leu Gly Asp Ala Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys		
30 35 40		
UCC CUA AGG GGA AGA GGC AGU ACU CUC GGU CUG AAC AUC GAA ACA GCC		197
Ser Leu Arg Gly Arg Gly Ser Thr Leu Gly Leu Asn Ile Glu Thr Ala		
45 50 55		
ACC CGU GUU GGA AAG CAG AUA GUG GAG AGG AUU CUG AAG GAA GAA UCC		245
Thr Arg Val Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser		
60 65 70		
GAU GAG GCA CUU AAA AUG ACC AUG GCC UCC GCA CCU GCU UCG CGA UAC		293
Asp Glu Ala Leu Lys Met Thr Met Ala Ser Ala Pro Ala Ser Arg Tyr		
75 80 85		
CUA ACU GAC AUG ACU AUU GAG GAA AUG UCA AGG GAC UGG UUC AUG CUA		341
Leu Thr Asp Met Thr Ile Glu Glu Met Ser Arg Asp Trp Phe Met Leu		
90 95 100 105		
AUG CCC AAG CAG AAA GUG GCA GGC CCU CUU UGU AUC AGA AUG GAC CAG		389
Met Pro Lys Gln Lys Val Ala Gly Pro Leu Cys Ile Arg Met Asp Gln		
110 115 120		
GCA AUC AUG GAU AAG AAC AUC AUA UUG AAA GCG AAU UUC AGU GUG AUU		437
Ala Ile Met Asp Lys Asn Ile Ile Leu Lys Ala Asn Phe Ser Val Ile		
125 130 135		
UUU GAC CGG CUA GAG ACC CUA AUA UUA CUA AGG GCU UUC ACC GAA ACG		485
Phe Asp Arg Leu Glu Thr Leu Ile Leu Leu Arg Ala Phe Thr Glu Thr		
140 145 150		
GGA GCA AUU GUU GGC GAA AUU UCA CCA UUG CCU UCU CUU CCA GGA CAU		533
Gly Ala Ile Val Gly Glu Ile Ser Pro Leu Pro Ser Leu Pro Gly His		
155 160 165		
ACU AAU GAG GAU GUC AAA AAU GCA AUU GGG GUC CUC AUC GGA GGA CUU		581
Thr Asn Glu Asp Val Lys Asn Ala Ile Gly Val Leu Ile Gly Gly Leu		
170 175 180 185		

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GAA UGG AAU GAU AAC ACA GUU CGA GUC UCU AAA ACU CUA CAG AGA UUC Glu Trp Asn Asp Asn Thr Val Arg Val Ser Lys Thr Leu Gln Arg Phe 190 195 200	629
GCU UGG AGA AGC AGU GAU GAG AAU GGG AGA CCU CCA CUC ACU CCA AAA Ala Trp Arg Ser Ser Asp Glu Asn Gly Arg Pro Pro Leu Thr Pro Lys 205 210 215	677
UAGAAACGGA AAAUGGCGAG AACAAUUAGG UCAAAAGUUC GAAGAAAUAA GAUGGCUGAU	737
UGAAGAAGUG AGACACAAAU UGAAGAUAAAC AGAGAAUAGU UUUGAGCAAA UAACAUUUUAU	797
GCAAGCCUUA CAGCUGCUAU UUGAAGUGGA ACAAGAGAUU AGAACUUUCU CGUUUCAGCU	857
UAUUUAAUGA UAAAAAACAC CCUUGUUUCU ACU	890

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu Trp 1 5 10 15
His Val Arg Lys Gln Val Ala Asp Gln Glu Leu Gly Asp Ala Pro Phe 20 25 30
Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly Arg Gly Ser 35 40 45
Thr Leu Gly Leu Asn Ile Glu Thr Ala Thr Arg Val Gly Lys Gln Ile 50 55 60
Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu Ala Leu Lys Met Thr 65 70 75 80
Met Ala Ser Ala Pro Ala Ser Arg Tyr Leu Thr Asp Met Thr Ile Glu 85 90 95
Glu Met Ser Arg Asp Trp Phe Met Leu Met Pro Lys Gln Lys Val Ala 100 105 110
Gly Pro Leu Cys Ile Arg Met Asp Gln Ala Ile Met Asp Lys Asn Ile 115 120 125
Ile Leu Lys Ala Asn Phe Ser Val Ile Phe Asp Arg Leu Glu Thr Leu 130 135 140
Ile Leu Leu Arg Ala Phe Thr Glu Thr Gly Ala Ile Val Gly Glu Ile 145 150 155 160
Ser Pro Leu Pro Ser Leu Pro Gly His Thr Asn Glu Asp Val Lys Asn 165 170 175
Ala Ile Gly Val Leu Ile Gly Gly Leu Glu Trp Asn Asp Asn Thr Val

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180

185

190

Arg Val Ser Lys Thr Leu Gln Arg Phe Ala Trp Arg Ser Ser Asp Glu
195 200 205

Asn Gly Arg Pro Pro Leu Thr Pro Lys
210 215

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 418 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 27..389

(D) OTHER INFORMATION: /product= "Nonstructural protein 2"
/gene= "NS2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCAAAAGCA GGGUGACAAA GACAUA AUG GAU CCU AAC ACU GUG UCA AGC UUU	53
Met Asp Pro Asn Thr Val Ser Ser Phe	
1 5	
CAG GAC AUA CUA AUG AGG AUG UCA AAA AUG CAA UUG GGG UCC UCA UCG	101
Gln Asp Ile Leu Met Arg Met Ser Lys Met Gln Leu Gly Ser Ser Ser	
10 15 20 25	
GAG GAC UUG AAU GGA AUG AUA ACA CAG UUC GAG UCU CUA AAA CUC UAC	149
Glu Asp Leu Asn Gly Met Ile Thr Gln Phe Glu Ser Leu Lys Leu Tyr	
30 35 40	
AGA GAU UCG CUU GGA GAA GCA GUG AUG AGA AUG GGA GAC CUC CAC UCA	197
Arg Asp Ser Leu Gly Glu Ala Val Met Arg Met Gly Asp Leu His Ser	
45 50 55	
CUC CAA AAU AGA AAC GGA AAA UGG CGA GAA CAA UUA GGU CAA AAG UUC	245
Leu Gln Asn Arg Asn Gly Lys Trp Arg Glu Gln Leu Gly Gln Lys Phe	
60 65 70	
GAA GAA AUA AGA UGG CUG AUU GAA GAA GUG AGA CAC AAA UUG AAG AUA	293
Glu Glu Ile Arg Trp Leu Ile Glu Glu Val Arg His Lys Leu Lys Ile	
75 80 85	
ACA GAG AAU AGU UUU GAG CAA AUA ACA UUU AUG CAA GCC UUA CAG CUG	341
Thr Glu Asn Ser Phe Glu Gln Ile Thr Phe Met Gln Ala Leu Gln Leu	
90 95 100 105	
CUA UUU GAA GUG GAA CAA GAG AUA AGA ACU UUC UCG UUU CAG CUU AUU	389
Leu Phe Glu Val Glu Gln Glu Ile Arg Thr Phe Ser Phe Gln Leu Ile	
110 115 120	
UAAUGAUA AAA AACACCCUU GUUUCUACU	418

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Asp Pro Asn Thr Val Ser Ser Phe Gln Asp Ile Leu Met Arg Met
 1          5          10          15
Ser Lys Met Gln Leu Gly Ser Ser Ser Glu Asp Leu Asn Gly Met Ile
          20          25          30
Thr Gln Phe Glu Ser Leu Lys Leu Tyr Arg Asp Ser Leu Gly Glu Ala
          35          40          45
Val Met Arg Met Gly Asp Leu His Ser Leu Gln Asn Arg Asn Gly Lys
          50          55          60
Trp Arg Glu Gln Leu Gly Gln Lys Phe Glu Glu Ile Arg Trp Leu Ile
          65          70          75          80
Glu Glu Val Arg His Lys Leu Lys Ile Thr Glu Asn Ser Phe Glu Gln
          85          90          95
Ile Thr Phe Met Gln Ala Leu Gln Leu Leu Phe Glu Val Glu Gln Glu
          100          105          110
Ile Arg Thr Phe Ser Phe Gln Leu Ile
          115          120

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: M

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 26..51
- (D) OTHER INFORMATION: /product= "matrix protein M2"
/gene= "M"
/note= "matrix protein M2"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: exon

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(B) LOCATION: 740..1004
 (D) OTHER INFORMATION: /product= "matrix protein M2"
 / gene= "M"
 / note= "matrix protein M2"
 / citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict
 (B) LOCATION: replace(969, "u")
 (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3)"
 / citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: join(26..51, 740..1004)
 (D) OTHER INFORMATION: /product= "matrix protein M2"
 / gene= "M"
 / note= "matrix protein M2"
 / citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 26..781
 (D) OTHER INFORMATION: /product= "matrix protein M1"
 / gene= "M"
 / note= "matrix protein M1"
 / citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
 Maassab, H F
 Webster, R G
 (B) TITLE: Molecular and biological changes in the cold
 adapted master strain A/AA/6/60 (H2N2) influenza
 virus
 (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
 (G) DATE: 1993
 (K) RELEVANT RESIDUES IN SEQ ID NO:5: FROM 1 TO 1027

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
 Kitame, F
 Kendal, A P
 Maassab, H F
 Naeve, C
 (B) TITLE: Identification of sequence changes in the
 cold-adapted live attenuated influenza vaccine
 strain, A/Ann Arbor/6/60(H2N2)
 (C) JOURNAL: Virology
 (D) VOLUME: 167
 (F) PAGES: 554-557
 (G) DATE: 1988
 (K) RELEVANT RESIDUES IN SEQ ID NO:5: FROM 1 TO 1027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGCAAAAGCA	GGUAGAUUU	GAAAG	AUG	AGU	CUU	CUA	ACC	GAG	GUC	GAA	ACG	52
			Met	Ser	Leu	Leu	Thr	Glu	Val	Glu	Thr	
			1				5					

UAC	GUU	CUC	UCU	AUC	AUC	CCG	UCA	GGC	CCC	CUC	AAA	GCC	GAG	AUC	GCA	100

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Tyr 10	Val	Leu	Ser	Ile	Ile 15	Pro	Ser	Gly	Pro	Leu 20	Lys	Ala	Glu	Ile	Ala 25	
CAG Gln	AGA Arg	CUU Leu	GAA Glu	GAU Asp 30	GUC Val	UUU Phe	GCU Ala	GGG Gly 35	AAA Lys	AAC Asn	ACC Thr	GAU Asp	CUU Leu 40	GAG Glu	GCU Ala	148
CUC Leu	AUG Met	GAA Glu	UGG Trp 45	CUA Leu	AAG Lys	ACA Thr	AGA Arg	CCA Pro 50	AUC Ile	CUG Leu	UCA Ser	CCU Pro	CUG Leu 55	ACU Thr	AAG Lys	196
GGG Gly	AUU Ile	UUG Leu 60	GGA Gly	UUU Phe	GUA Val	UUC Phe	ACG Thr 65	CUC Leu	ACC Thr	GUG Val	CCC Pro	AGU Ser 70	GAG Glu	CGA Arg	GGA Gly	244
CUG Leu	CAG Gln 75	CGU Arg	AGA Arg	CGC Arg	UUU Phe	GUC Val 80	CAA Gln	AAU Asn	GCC Ala	CUC Leu	AAU Asn 85	GGG Gly	AAU Asn	GGG Gly	GAU Asp	292
CCA Pro 90	AAU Asn	AAC Asn	AUG Met	GAC Asp	AGA Arg 95	GCA Ala	GUU Val	AAA Lys	CUG Leu	UAU Tyr 100	AGA Arg	AAG Lys	CUU Leu	AAG Lys	AGG Arg 105	340
GAG Glu	AUA Ile	ACA Thr	UUC Phe	CAU His 110	GGG Gly	GCC Ala	AAA Lys	GAA Glu	AUA Ile 115	GCG Ala	CUC Leu	AGU Ser	UAU Tyr	UCU Ser 120	GCU Ala	388
GGU Gly	GCA Ala	CUU Leu	GCC Ala 125	AGU Ser	UGU Cys	AUG Met	GGC Gly 130	CUC Leu	AUA Ile	UAC Tyr	AAC Asn	AGG Arg	AUG Met 135	GGG Gly	GCU Ala	436
GUG Val	ACC Thr	ACU Thr 140	GAA Glu	GUG Val	GUC Val	UUA Leu	GGC Gly 145	CUG Leu	GUA Val	UGU Cys	GCA Ala	ACC Thr 150	UGU Cys	GAA Glu	CAG Gln	484
AUU Ile 155	GCU Ala	GAC Asp	UCC Ser	CAG Gln	CAU His	AGG Arg 160	UCU Ser	CAU His	AGG Arg	CAA Gln	AUG Met 165	GUG Val	ACA Thr	ACA Thr	ACC Thr	532
AAU Asn 170	CCA Pro	CUA Leu	AUA Ile	AGA Arg	CAU His 175	GAG Glu	AAC Asn	AGA Arg	AUG Met	GUU Val 180	CUG Leu	GCC Ala	AGC Ser	ACU Thr	ACA Thr 185	580
GCU Ala	AAG Lys	GCU Ala	AUG Met	GAG Glu 190	CAA Gln	AUG Met	GCU Ala	GGA Gly	UCG Ser 195	AGU Ser	GAG Glu	CAA Gln	GCA Ala	GCA Ala 200	GAG Glu	628
GCC Ala	AUG Met	GAG Glu	GUU Val 205	GCU Ala	AGU Ser	CAG Gln	GCC Ala	AGG Arg 210	CAA Gln	AUG Met	GUG Val	CAG Gln	GCA Ala 215	AUG Met	AGA Arg	676
GUU Val	AUU Ile	GGG Gly 220	ACU Thr	CAU His	CCU Pro	AGC Ser	UCC Ser 225	AGU Ser	GCU Ala	GGU Gly	CUA Leu	AAA Lys 230	AAU Asn	GAU Asp	CUU Leu	724
CUU Leu 235	GAA Glu	AAU Asn	UUG Leu	CAG Gln	GCC Ala	UAU Tyr 240	CAG Gln	AAA Lys	CGA Arg	AUG Met	GGG Gly 245	GUG Val	CAG Gln	AUG Met	CAA Gln	772
CGA Arg 250	UUC Phe	AAG Lys	UGACCCUCUU GUUGUUGCCG CGAGUAUCAU UGGGAUCUUG													821

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CACUUGAUU	UGUGGAUUCU	UGAUCAUUU	UUUUUCAAU	GCAUUUAUCG	CUUCUUUAAA	881
CACGGUCUGA	AAAGAGGGCC	UUCUACGGAA	GGAGUACCAG	AGUCUAUGAG	GGAAGAAU	941
CGAAAGGAAC	AGCAGAGUGC	UGUGGAUUCU	GACGAUAGUC	AUUUUGUCAG	CAUAGAGCUG	1001
GAGUAAAAA	CUACCUUGUU	UCUACU				1027

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Leu	Leu	Thr	Glu	Val	Glu	Thr	Tyr	Val	Leu	Ser	Ile	Ile	Pro
1				5				10						15	
Ser	Gly	Pro	Leu	Lys	Ala	Glu	Ile	Ala	Gln	Arg	Leu	Glu	Asp	Val	Phe
			20					25					30		
Ala	Gly	Lys	Asn	Thr	Asp	Leu	Glu	Ala	Leu	Met	Glu	Trp	Leu	Lys	Thr
		35					40					45			
Arg	Pro	Ile	Leu	Ser	Pro	Leu	Thr	Lys	Gly	Ile	Leu	Gly	Phe	Val	Phe
	50					55					60				
Thr	Leu	Thr	Val	Pro	Ser	Glu	Arg	Gly	Leu	Gln	Arg	Arg	Arg	Phe	Val
65				70				75							80
Gln	Asn	Ala	Leu	Asn	Gly	Asn	Gly	Asp	Pro	Asn	Asn	Met	Asp	Arg	Ala
			85					90						95	
Val	Lys	Leu	Tyr	Arg	Lys	Leu	Lys	Arg	Glu	Ile	Thr	Phe	His	Gly	Ala
		100						105					110		
Lys	Glu	Ile	Ala	Leu	Ser	Tyr	Ser	Ala	Gly	Ala	Leu	Ala	Ser	Cys	Met
	115					120					125				
Gly	Leu	Ile	Tyr	Asn	Arg	Met	Gly	Ala	Val	Thr	Thr	Glu	Val	Val	Leu
	130					135					140				
Gly	Leu	Val	Cys	Ala	Thr	Cys	Glu	Gln	Ile	Ala	Asp	Ser	Gln	His	Arg
145				150				155							160
Ser	His	Arg	Gln	Met	Val	Thr	Thr	Thr	Asn	Pro	Leu	Ile	Arg	His	Glu
			165					170						175	
Asn	Arg	Met	Val	Leu	Ala	Ser	Thr	Thr	Ala	Lys	Ala	Met	Glu	Gln	Met
		180					185					190			
Ala	Gly	Ser	Ser	Glu	Gln	Ala	Ala	Glu	Ala	Met	Glu	Val	Ala	Ser	Gln
	195					200						205			
Ala	Arg	Gln	Met	Val	Gln	Ala	Met	Arg	Val	Ile	Gly	Thr	His	Pro	Ser
	210				215					220					
Ser	Ser	Ala	Gly	Leu	Lys	Asn	Asp	Leu	Leu	Glu	Asn	Leu	Gln	Ala	Tyr

225 230 235 240
 Gln Lys Arg Met Gly Val Gln Met Gln Arg Phe Lys
 245 250

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 26..316
- (D) OTHER INFORMATION: /product= "Matrix M2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGCAAAAGCA GGUAGAUUU GAAAG	AUG AGU CUU CUA ACC GAG GUC GAA ACG	52
	Met Ser Leu Leu Thr Glu Val Glu Thr	
	1 5	
CCU AUC AGA AAC GAA UGG GGG UGC AGA UGC AAC GAU UCA AGU GAC CCU		100
Pro Ile Arg Asn Glu Trp Gly Cys Arg Cys Asn Asp Ser Ser Asp Pro		
10 15 20 25		
CUU GUU GUU GCC GCG AGU AUC AUU GGG AUC UUG CAC UUG AUA UUG UGG		148
Leu Val Val Ala Ala Ser Ile Ile Gly Ile Leu His Leu Ile Leu Trp		
	30 35 40	
AUU CUU GAU CAU CUU UUU UUC AAA UGC AUU UAU CGC UUC UUU AAA CAC		196
Ile Leu Asp His Leu Phe Phe Lys Cys Ile Tyr Arg Phe Phe Lys His		
	45 50 55	
GGU CUG AAA AGA GGG CCU UCU ACG GAA GGA GUA CCA GAG UCU AUG AGG		244
Gly Leu Lys Arg Gly Pro Ser Thr Glu Gly Val Pro Glu Ser Met Arg		
	60 65 70	
GAA GAA UAU CGA AAG GAA CAG CAG AGU GCU GUG GAU UCU GAC GAU AGU		292
Glu Glu Tyr Arg Lys Glu Gln Gln Ser Ala Val Asp Ser Asp Asp Ser		
	75 80 85	
CAU UUU GUC AGC AUA GAG CUG GAG UAAAAACUA CCUUGUUUCU ACU		339
His Phe Val Ser Ile Glu Leu Glu		
	90 95	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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```

Met Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly
 1           5           10           15
Cys Arg Cys Asn Asp Ser Ser Asp Pro Leu Val Val Ala Ala Ser Ile
          20           25           30
Ile Gly Ile Leu His Leu Ile Leu Trp Ile Leu Asp His Leu Phe Phe
 35           40           45
Lys Cys Ile Tyr Arg Phe Phe Lys His Gly Leu Lys Arg Gly Pro Ser
 50           55           60
Thr Glu Gly Val Pro Glu Ser Met Arg Glu Glu Tyr Arg Lys Glu Gln
 65           70           75           80
Gln Ser Ala Val Asp Ser Asp Asp Ser His Phe Val Ser Ile Glu Leu
          85           90           95
Glu

```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: NP

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(113, "c")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain; a in wt2(3); a in 1988 reported ca vaccine strain (manuscript), but c reported in 1988 genbank"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(146, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(627, "c")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain and in wt2(3); a in 1988 reported ca vaccine strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict

09573569 Sequence Listing.txt

(B) LOCATION: replace(909, "g")
 (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3);
 c in 1988 reported ca vaccine strain"
 /citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict
 (B) LOCATION: replace(1550, "a")
 (D) OTHER INFORMATION: /note= "a in ca "master" strain and in wt2(3)"
 /citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 46..1539
 (D) OTHER INFORMATION: /product= "Nucleoprotein"
 /gene= "NP"
 /note= "nucleoprotein"
 /citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
 Maassab, H F
 Webster, R W
 (B) TITLE: Molecular and biological changes in the cold
 adapted master strain A/AA/6/60 (H2N2) influenza
 virus
 (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
 (G) DATE: 1993
 (K) RELEVANT RESIDUES IN SEQ ID NO:9: FROM 1 TO 1566

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
 Kitame, F
 Kendal, A P
 Maassab, H F
 Naeve, C
 (B) TITLE: Identification of sequence changes in the
 cold-adapted live attenuated influenza vaccine
 strain, A/Ann Arbor/6/60 (H2N2)
 (C) JOURNAL: Virology
 (D) VOLUME: 167
 (F) PAGES: 554-567
 (G) DATE: 1988
 (K) RELEVANT RESIDUES IN SEQ ID NO:9: FROM 1 TO 1566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGCAAAAGCA GGGUAGAUAA UCACUCACUG AGUGACAUCA AAAUC AUG GCG UCC	54
Met Ala Ser	
1	
CAA GGC ACC AAA CGG UCU UAU GAA CAG AUG GAA ACU GAU GGG GAA CGC	102
Gln Gly Thr Lys Arg Ser Tyr Glu Gln Met Glu Thr Asp Gly Glu Arg	
5 10 15	
CAG AAU GCA ACU GAA AUC AGA GCA UCC GUC GGG AAG AUG AUU GGU GGA	150
Gln Asn Ala Thr Glu Ile Arg Ala Ser Val Gly Lys Met Ile Gly Gly	
20 25 30 35	
AUU GGA CGA UUC UAC AUC CAA AUG UGC ACC GAA CUU AAA CUC AGU GAU	198
Ile Gly Arg Phe Tyr Ile Gln Met Cys Thr Glu Leu Lys Leu Ser Asp	
40 45 50	

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UAU GAG GGG CGG CUG AUC CAG AAC AGC UUA ACA AUA GAG AGA AUG GUG Tyr Glu Gly Arg 55 Leu Ile Gln Asn Ser 60 Leu Thr Ile Glu Arg 65 Met Val	246
CUC UCU GCU UUU GAC GAG AGG AGG AAU AAA UAU CUG GAA GAA CAU CCC Leu Ser Ala 70 Phe Asp Glu Arg Arg 75 Asn Lys Tyr Leu Glu 80 Glu His Pro	294
AGC GCG GGG AAG GAU CCU AAG AAA ACU GGA GGA CCC AUA UAC AAG AGA Ser Ala 85 Gly Lys Asp Pro Lys 90 Lys Thr Gly Gly Pro 95 Ile Tyr Lys Arg	342
GUA GAU GGA AAG UGG AUG AGG GAA CUC GUC CUU UAU GAC AAA GAA GAA Val 100 Asp Gly Lys Trp Met 105 Arg Glu Leu Val 110 Leu Tyr Asp Lys Glu 115 Glu	390
AUA AGG CGA AUC UGG CGC CAA GCU AAU AAU GGU GAU GAU GCA ACA GCU Ile Arg Arg Ile Trp 120 Arg Gln Ala Asn 125 Asn Gly Asp Asp Ala Thr 130 Ala	438
GGU CUG ACU CAC AUG AUG AUC UGG CAU UCC AAU UUG AAU GAU ACA ACA Gly Leu Thr His 135 Met Met Ile Trp His 140 Ser Asn Leu Asn 145 Asp Thr Thr	486
UAC CAG AGG ACA AGA GCU CUU GUU CGC ACC GGA AUG GAU CCC AGG AUG Tyr Gln Arg 150 Thr Arg Ala Leu Val 155 Arg Thr Gly Met Asp 160 Pro Arg Met	534
UGC UCU UUG AUG CAG GGU UCG ACU CUC CCU AGG AGG UCU GGA GCC GCA Cys Ser 165 Leu Met Gln Gly Ser 170 Thr Leu Pro Arg Arg 175 Ser Gly Ala Ala	582
GGC GCU GCA GUC AAA GGA GUU GGG ACA AUG GUG AUG GAG UUG AUC AGG Gly Ala Ala Val Lys 185 Gly Val Gly Thr Met Val 190 Met Glu Leu Ile Arg 195 Arg	630
AUG AUC AAA CGU GGG AUC AAU GAU CGG AAC UUC UGG AGA GGU GAG AAU Met Ile Lys Arg 200 Gly Ile Asn Asp Arg 205 Asn Phe Trp Arg Gly Glu 210 Asn	678
GGG CGG AAA ACA AGG AAU GCU UAU GAG AGA AUG UGC AAC AUU CUC AAA Gly Arg Lys Thr 215 Arg Asn Ala Tyr Glu 220 Arg Met Cys Asn 225 Ile Leu Lys	726
GGA AAA UUU CAA ACA GCU GCA CAA AGA GCA AUG AUG GAU CAA GUG AGA Gly Lys Phe 230 Gln Thr Ala Ala Gln Arg Ala Met Met Asp 240 Gln Val Arg	774
GAA AGC CGG AAC CCA GGA AAU GCU GAG AUC GAA GAU CUC AUC UUU CUG Glu Ser 245 Arg Asn Pro Gly Asn 250 Ala Glu Ile Glu Asp 255 Leu Ile Phe Leu	822
GCA CGG UCU GCA CUC AUA UUG AGA GGG UCA GUU GCU CAC AAA UCU UGU Ala Arg Ser Ala Leu Ile 265 Leu Arg Gly Ser Val 270 Ala His Lys Ser Cys 275	870
CUG CCU GCC UGU GUG UAU GGA CCU GCC GUA GCC AGU GGG UAC GAC UUC Leu Pro Ala Cys Val Tyr Gly Pro Ala Val 285 Ala Ser Gly Tyr Asp 290 Phe	918
GAA AAA GAG GGA UAC UCU UUA GUA GGG AUA GAC CCU UUC AAA CUG CUU Glu Lys Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe Lys Leu Leu	966

09573569 Sequence Listing.txt

295	300	305	
CAA AAC AGC CAA GUA UAC AGC CUA AUC AGA CCG AAU GAG AAU CCA GCA Gln Asn Ser Gln Val Tyr Ser Leu Ile Arg Pro Asn Glu Asn Pro Ala 310 315 320			1014
CAC AAG AGU CAG CUG GUG UGG AUG GCA UGC AAU UCU GCU GCA UUU GAA His Lys Ser Gln Leu Val Trp Met Ala Cys Asn Ser Ala Ala Phe Glu 325 330 335			1062
GAU CUA AGA GUA UCA AGC UUC AUC AGA GGG ACC AAA GUA AUC CCA AGG Asp Leu Arg Val Ser Ser Phe Ile Arg Gly Thr Lys Val Ile Pro Arg 340 345 350 355			1110
GGG AAA CUU UCC ACU AGA GGA GUA CAA AUU GCU UCA AAU GAA AAC AUG Gly Lys Leu Ser Thr Arg Gly Val Gln Ile Ala Ser Asn Glu Asn Met 360 365 370			1158
GAU ACU AUG GGA UCA AGU ACU CUU GAA CUG AGA AGC AGG UAC UGG GCC Asp Thr Met Gly Ser Ser Thr Leu Glu Leu Arg Ser Arg Tyr Trp Ala 375 380 385			1206
AUA AGG ACC AGA AGU GGA GGA AAC ACU AAU CAA CAG AGG GCC UCU GCA Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg Ala Ser Ala 390 395 400			1254
GGU CAA AUC AGU GUA CAA CCU ACG UUU UCU GUG CAA AGA AAC CUC CCA Gly Gln Ile Ser Val Gln Pro Thr Phe Ser Val Gln Arg Asn Leu Pro 405 410 415			1302
UUU GAC AAA CCA ACC AUC AUG GCA GCA UUC ACU GGG AAU GCA GAG GGA Phe Asp Lys Pro Thr Ile Met Ala Ala Phe Thr Gly Asn Ala Glu Gly 420 425 430 435			1350
AGA ACA UCA GAC AUG AGG GCA GAA AUC AUA AGG AUG AUG GAA GGU GCA Arg Thr Ser Asp Met Arg Ala Glu Ile Ile Arg Met Met Glu Gly Ala 440 445 450			1398
AAA CCA GAA GAA GUG UCC UUC CAG GGG CGG GGA GUC UUC GAG CUC UCG Lys Pro Glu Glu Val Ser Phe Gln Gly Arg Gly Val Phe Glu Leu Ser 455 460 465			1446
GAC GAA AAG GCA ACG AAC CCG AUC GUG CCC UCU UUU GAC AUG AGU AAU Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp Met Ser Asn 470 475 480			1494
GAA GGA UCU UAU UUC UUC GGA GAC AAU GCA GAG GAG UAC GAC AAU Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr Asp Asn 485 490 495			1539
UAAGGAAAAA AUACCCUUGU UUCUACU			1566

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

09573569 Sequence Listing.txt

Met Ala Ser Gln Gly Thr Lys Arg Ser Tyr Glu Gln Met Glu Thr Asp
1 5 10 15
Gly Glu Arg Gln Asn Ala Thr Glu Ile Arg Ala Ser Val Gly Lys Met
20 25 30
Ile Gly Gly Ile Gly Arg Phe Tyr Ile Gln Met Cys Thr Glu Leu Lys
35 40 45
Leu Ser Asp Tyr Glu Gly Arg Leu Ile Gln Asn Ser Leu Thr Ile Glu
50 55 60
Arg Met Val Leu Ser Ala Phe Asp Glu Arg Arg Asn Lys Tyr Leu Glu
65 70 75 80
Glu His Pro Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Gly Pro Ile
85 90 95
Tyr Lys Arg Val Asp Gly Lys Trp Met Arg Glu Leu Val Leu Tyr Asp
100 105 110
Lys Glu Glu Ile Arg Arg Ile Trp Arg Gln Ala Asn Asn Gly Asp Asp
115 120 125
Ala Thr Ala Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn
130 135 140
Asp Thr Thr Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp
145 150 155 160
Pro Arg Met Cys Ser Leu Met Gln Gly Ser Thr Leu Pro Arg Arg Ser
165 170 175
Gly Ala Ala Gly Ala Ala Val Lys Gly Val Gly Thr Met Val Met Glu
180 185 190
Leu Ile Arg Met Ile Lys Arg Gly Ile Asn Asp Arg Asn Phe Trp Arg
195 200 205
Gly Glu Asn Gly Arg Lys Thr Arg Asn Ala Tyr Glu Arg Met Cys Asn
210 215 220
Ile Leu Lys Gly Lys Phe Gln Thr Ala Ala Gln Arg Ala Met Met Asp
225 230 235 240
Gln Val Arg Glu Ser Arg Asn Pro Gly Asn Ala Glu Ile Glu Asp Leu
245 250 255
Ile Phe Leu Ala Arg Ser Ala Leu Ile Leu Arg Gly Ser Val Ala His
260 265 270
Lys Ser Cys Leu Pro Ala Cys Val Tyr Gly Pro Ala Val Ala Ser Gly
275 280 285
Tyr Asp Phe Glu Lys Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe
290 295 300
Lys Leu Leu Gln Asn Ser Gln Val Tyr Ser Leu Ile Arg Pro Asn Glu
305 310 315 320
Asn Pro Ala His Lys Ser Gln Leu Val Trp Met Ala Cys Asn Ser Ala
325 330 335

09573569 Sequence Listing.txt

Ala Phe Glu Asp Leu Arg Val Ser Ser Phe Ile Arg Gly Thr Lys Val
340 345 350
Ile Pro Arg Gly Lys Leu Ser Thr Arg Gly Val Gln Ile Ala Ser Asn
355 360 365
Glu Asn Met Asp Thr Met Gly Ser Ser Thr Leu Glu Leu Arg Ser Arg
370 375 380
Tyr Trp Ala Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg
385 390 395 400
Ala Ser Ala Gly Gln Ile Ser Val Gln Pro Thr Phe Ser Val Gln Arg
405 410 415
Asn Leu Pro Phe Asp Lys Pro Thr Ile Met Ala Ala Phe Thr Gly Asn
420 425 430
Ala Glu Gly Arg Thr Ser Asp Met Arg Ala Glu Ile Ile Arg Met Met
435 440 445
Glu Gly Ala Lys Pro Glu Glu Val Ser Phe Gln Gly Arg Gly Val Phe
450 455 460
Glu Leu Ser Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp
465 470 475 480
Met Ser Asn Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr
485 490 495
Asp Asn

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PA

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(20, "c")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(75, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3);
u in 1988 reported ca vaccine strain"

09573569 Sequence Listing.txt
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict
(B) LOCATION: replace(1861, "g")
(D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict
(B) LOCATION: replace(2167..2168, "cc")
(D) OTHER INFORMATION: /note= "cc in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 25..2172
(D) OTHER INFORMATION: /product= "polymerase acidic
protein"
/gene= "PA"
/note= "polymerase acidic protein"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
(B) TITLE: Molecular and biological changes in the cold
adapted master strain A/AA/6/60 (H2N2) influenza
virus
(C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
(G) DATE: 1993
(K) RELEVANT RESIDUES IN SEQ ID NO:11: FROM 1 TO 2233

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C
(B) TITLE: Identification of sequence changes in the
cold-adapted live attenuated influenza strain,
A/Ann Arbor/6/60(H2N2)
(C) JOURNAL: Virology
(D) VOLUME: 167
(F) PAGES: 554-567
(G) DATE: 1988
(K) RELEVANT RESIDUES IN SEQ ID NO:11: FROM 1 TO 2233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCGAAAGCA GGUACUGAUC CGAA AUG GAA GAU UUU GUG CGA CAA UGC UUC	51
Met Glu Asp Phe Val Arg Gln Cys Phe	
1 5	
AAU CCG AUG AUU GUC GAG CUU GCG GAA AAA GCA AUG AAA GAG UAU GGA	99
Asn Pro Met Ile Val Glu Leu Ala Glu Lys Ala Met Lys Glu Tyr Gly	
10 15 20 25	
GAG GAU CUG AAA AUC GAA ACA AAC AAA UUU GCA GCA AUA UGC ACU CAC	147
Glu Asp Leu Lys Ile Glu Thr Asn Lys Phe Ala Ala Ile Cys Thr His	
30 35 40	

09573569 Sequence Listing.txt

UUG GAA GUA UGC UUC AUG UAU UCA GAU UUU CAU UUC AUC AAU GAG CAA Leu Glu Val Cys Phe Met Tyr Ser Asp Phe His Phe Ile Asn Glu Gln 45 50 55	195
GGC GAG UCA AUA AUA GUA GAG CUU GAU GAU CCA AAU GCA CUU UUG AAG Gly Glu Ser Ile Ile Val Glu Leu Asp Asp Pro Asn Ala Leu Leu Lys 60 65 70	243
CAC AGA UUU GAA AUA AUA GAG GGA AGA GAU CGC ACA AUG GCC UGG ACA His Arg Phe Glu Ile Ile Glu Gly Arg Asp Arg Thr Met Ala Trp Thr 75 80 85	291
GUA GUA AAC AGU AUU UGC AAC ACU ACA GGA GCU GAG AAA CCG AAG UUU Val Val Asn Ser Ile Cys Asn Thr Thr Gly Ala Glu Lys Pro Lys Phe 90 95 100 105	339
CUG CCA GAU UUG UAU GAU UAC AAG GAG AAU AGA UUC AUC GAG AUU GGA Leu Pro Asp Leu Tyr Asp Tyr Lys Glu Asn Arg Phe Ile Glu Ile Gly 110 115 120	387
GUG ACA AGG AGG GAA GUC CAC AUA UAC UAU CUU GAA AAG GCC AAU AAA Val Thr Arg Arg Glu Val His Ile Tyr Tyr Leu Glu Lys Ala Asn Lys 125 130 135	435
AUU AAA UCU GAG AAG ACA CAC AUC CAC AUU UUC UCA UUC ACU GGG GAA Ile Lys Ser Glu Lys Thr His Ile His Ile Phe Ser Phe Thr Gly Glu 140 145 150	483
GAA AUG GCC ACA AAG GCC GAC UAC ACU CUC GAU GAG GAA AGC AGG GCU Glu Met Ala Thr Lys Ala Asp Tyr Thr Leu Asp Glu Glu Ser Arg Ala 155 160 165	531
AGG AUC AAA ACC AGA CUA UUC ACC AUA AGA CAA GAA AUG GCU AGC AGA Arg Ile Lys Thr Arg Leu Phe Thr Ile Arg Gln Glu Met Ala Ser Arg 170 175 180 185	579
GGC CUC UGG GAU UCC UUU CAU CAG UCC GAA AGA GGC GAA GAA ACA AUU Gly Leu Trp Asp Ser Phe His Gln Ser Glu Arg Gly Glu Glu Thr Ile 190 195 200	627
GAA GAA AGA UUU GAA AUC ACA GGG ACA AUG CGC AGG CUC GCC GAC CAA Glu Glu Arg Phe Glu Ile Thr Gly Thr Met Arg Arg Leu Ala Asp Gln 205 210 215	675
AGU CUC CCG CCG AAC UUC UCC UGC CUU GAG AAU UUU AGA GCC UAU GUG Ser Leu Pro Pro Asn Phe Ser Cys Leu Glu Asn Phe Arg Ala Tyr Val 220 225 230	723
GAU GGA UUC GAA CCG AAC GGC UAC AUU GAG GGC AAG CUU UCU CAA AUG Asp Gly Phe Glu Pro Asn Gly Tyr Ile Glu Gly Lys Leu Ser Gln Met 235 240 245	771
UCC AAA GAA GUA AAU GCU AAA AUU GAA CCU UUU CUG AAA ACA ACA CCA Ser Lys Glu Val Asn Ala Lys Ile Glu Pro Phe Leu Lys Thr Thr Pro 250 255 260 265	819
AGA CCA AUU AGA CUU CCG GAU GGG CCU CCU UGU UCU CAG CGG UCC AAA Arg Pro Ile Arg Leu Pro Asp Gly Pro Pro Cys Ser Gln Arg Ser Lys 270 275 280	867
UUC CUG CUG AUG GAU GCU UUA AAA UUA AGC AUU GAG GAC CCA AGU CAC Phe Leu Leu Met Asp Ala Leu Lys Leu Ser Ile Glu Asp Pro Ser His 285 290 295	915

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285	290	295	
GAA Glu	GGA Gly	GAG Glu 300	963
GGA Gly	AUA Ile	CCA Pro	
CUA Leu	UAU Tyr 305	GAU Asp	
GCG Ala	AUC Ile	AAG Lys	
UGU Cys 310	AUG Met	AGA Arg	
ACA Thr			
UUC Phe	UUU Phe 315	GGA Gly	1011
UGG Trp	AAA Lys	GAA Glu	
GAA Glu	CCC Pro 320	UUA Tyr	
GUU Val	GUU Val	AAA Lys	
CCA Pro 325	CAC His	AAG Lys	
GGA Gly			
AUA Ile 330	AAU Asn	CCA Pro	1059
AAU Asn	UAU Tyr	CUG Leu 335	
CUG Leu	CUG Leu	UCA Ser	
UGG Trp	AAG Lys	CAA Gln 340	
GUA Val	CUG Leu	GCA Ala	
GAA Glu	CUG Leu		
CUG Leu 345			
CAG Gln	GAC Asp	AUU Ile	1107
GAG Glu	AAU Asn 350	GAG Glu	
GAG Glu	AAG Lys	AUU Ile	
CCA Pro 355	AGA Arg	ACC Thr	
AAA Lys	AAC Asn	AUG Met 360	
AAG Lys			
AAA Lys	ACG Thr	AGU Ser	1155
CAG Gln 365	CUA Leu	AAG Lys	
UGG Trp	GCA Ala	CUU Leu 370	
GAG Glu	AAC Asn	AUG Met 375	
GCA Ala	CCA Pro	GAG Glu	
AAG Lys			
GUA Val	GAC Asp 380	UUU Phe	1203
GAC Asp	GAC Asp	UGU Cys	
AGA Arg 385	GAU Asp	GUA Val	
AGC Ser	GAU Asp	UUG Leu 390	
AAG Lys	CAA Gln	UAU Tyr	
GAU Asp	AGU Ser 395	GAU Asp	1251
GAA Glu	CCU Pro	GAA Glu	
CUU Leu 400	AGG Arg	UCA Ser	
CUU Leu	UCA Ser	AGC Ser 405	
UGG Trp	AUC Ile	CAG Gln	
AAU Asn			
GAG Glu 410	UUC Phe	AAC Asn	1299
AAG Lys	GCA Ala	UGC Cys 415	
GAG Glu	CUG Leu	ACC Thr	
GAU Asp	UCA Ser 420	AUC Ile	
UGG Trp	AUA Ile	GAG Glu	
CUC Leu 425			
GAU Asp	GAG Glu	AUU Ile	1347
GAA Glu	GAU Asp	GUG Val	
GCU Ala	CCA Pro	AUU Ile 435	
GAA Glu	CAC His	AUU Ile	
GCA Ala	AGC Ser 440	AUG Met	
AGA Arg	AGG Arg	AAU Asn 445	1395
UAC Tyr	UUC Phe	ACA Thr	
GCA Ala	GAG Glu	GUG Val 450	
UCU Ser	CAU His	UGC Cys	
AGA Arg	GCC Ala 455	ACA Thr	
GAA Glu			
UAU Tyr	AUA Ile 460	AAG Lys	1443
GGG Gly	GUA Val	UAC Tyr	
AAU Asn 465	AUU Ile	AAU Asn	
ACU Thr	GCC Ala	UUG Leu 470	
CUU Leu	AAU Asn	GCA Ala	
UCC Ser			
UGU Cys	GCA Ala 475	GCA Ala	1491
AUG Met	GAC Asp	GAU Asp	
UUC Phe 480	CAA Gln	CUA Leu	
AUU Ile 485	CCC Pro	AUG Met 485	
AUA Ile	AGC Ser	AAA Lys	
UGU Cys			
AGA Arg 490	ACU Thr	AAA Lys	1539
GAG Glu	GGA Gly	AGG Arg 495	
CGA Arg	AAG Lys	ACC Thr	
AAU Asn 500	UUA Leu	UAU Tyr	
GGU Gly	UUC Phe	AUC Ile 505	
AAA Lys	GGA Gly	AGA Arg	1587
AGU Ser	CAC His 510	UUA Leu	
AGG Arg	AAU Asn	GAC Asp 515	
ACC Thr	GAC Asp	GUG Val	
GUA Val	AAC Asn	UUU Phe 520	
GUG Val			
AGC Ser	AUG Met	GAG Glu	1635
UUU Phe 525	UCU Ser	CUC Leu	
ACU Thr	GAC Asp	CCA Pro 530	
AGA Arg	CUU Leu	GAG Glu	
CCA Pro 535	CAC His 535	AAA Lys	
UGG Trp			
GAG Glu	AAG Lys	UAC Tyr	1683
UGU Cys	GUU Val	CUU Leu	
GAG Glu	AUA Ile	GGA Gly	
GAU Asp	AUG Met	CUA Leu	
CUA Leu	AGA Arg	AGU Ser	
GCC Ala			

09573569 Sequence Listing.txt

Glu Lys Tyr Cys Val Leu Glu Ile Gly Asp Met Leu Leu Arg Ser Ala	
540 545 550	
AUA GGC CAG GUG UCA AGG CCC AUG UUC UUG UAU GUG AGG ACA AAU GGA	1731
Ile Gly Gln Val Ser Arg Pro Met Phe Leu Tyr Val Arg Thr Asn Gly	
555 560 565	
ACA UCA AAG AUU AAA AUG AAA UGG GGA AUG GAG AUG AGG CGU UGC CUC	1779
Thr Ser Lys Ile Lys Met Lys Trp Gly Met Glu Met Arg Arg Cys Leu	
570 575 580	
CUU CAG UCA CUC CAA CAA AUC GAG AGU AUG AUU GAA GCC GAG UCC UCU	1827
Leu Gln Ser Leu Gln Gln Ile Glu Ser Met Ile Glu Ala Glu Ser Ser	
590 595 600	
GUC AAG GAG AAA GAC AUG ACC AAA GAG UUU UUC GAG AAU AAA UCA GAA	1875
Val Lys Glu Lys Asp Met Thr Lys Glu Phe Phe Glu Asn Lys Ser Glu	
605 610 615	
ACA UGG CCC AUU GGA GAG UCC CCC AAA GGA GUG GAA GAA GGU UCC AUU	1923
Thr Trp Pro Ile Gly Glu Ser Pro Lys Gly Val Glu Glu Gly Ser Ile	
620 625 630	
GGG AAG GUC UGC AGG ACU UUA UUA GCC AAG UCG GUA UUC AAU AGC CUG	1971
Gly Lys Val Cys Arg Thr Leu Leu Ala Lys Ser Val Phe Asn Ser Leu	
635 640 645	
UAU GCA UCU CCA CAA UUA GAA GGA UUU UCA GCU GAA UCA AGA AAA CUG	2019
Tyr Ala Ser Pro Gln Leu Glu Gly Phe Ser Ala Glu Ser Arg Lys Leu	
650 655 660	
CUU CUU GUC GUU CAG GCU CUU AGG GAC AAU CUU GAA CCU GGG ACC UUU	2067
Leu Leu Val Val Gln Ala Leu Arg Asp Asn Leu Glu Pro Gly Thr Phe	
670 675 680	
GAU CUU GGG GGG CUA UAU GAA GCA AUU GAG GAG UGC CUG AUU AAU GAU	2115
Asp Leu Gly Gly Leu Tyr Glu Ala Ile Glu Glu Cys Leu Ile Asn Asp	
685 690 695	
CCC UGG GUU UUG CUU AAU GCG UCU UGG UUC AAC UCC UUC CUA ACA CAU	2163
Pro Trp Val Leu Leu Asn Ala Ser Trp Phe Asn Ser Phe Leu Thr His	
700 705 710	
GCA CCA AGA UAGUUGUGGC AAUGCUACUA UUUGCUAUCC AUACUGUCCA	2212
Ala Pro Arg	
715	
AAAAAGUACC UUGUUUCUAC U	2233

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 716 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Glu Asp Phe Val Arg Gln Cys Phe Asn Pro Met Ile Val Glu Leu
1 5 10 15

09573569 Sequence Listing.txt

Ala Glu Lys Ala Met Lys Glu Tyr Gly Glu Asp Leu Lys Ile Glu Thr
20 25 30
Asn Lys Phe Ala Ala Ile Cys Thr His Leu Glu Val Cys Phe Met Tyr
35 40 45
Ser Asp Phe His Phe Ile Asn Glu Gln Gly Glu Ser Ile Ile Val Glu
50 55 60
Leu Asp Asp Pro Asn Ala Leu Leu Lys His Arg Phe Glu Ile Ile Glu
65 70 75 80
Gly Arg Asp Arg Thr Met Ala Trp Thr Val Val Asn Ser Ile Cys Asn
85 90 95
Thr Thr Gly Ala Glu Lys Pro Lys Phe Leu Pro Asp Leu Tyr Asp Tyr
100 105 110
Lys Glu Asn Arg Phe Ile Glu Ile Gly Val Thr Arg Arg Glu Val His
115 120 125
Ile Tyr Tyr Leu Glu Lys Ala Asn Lys Ile Lys Ser Glu Lys Thr His
130 135 140
Ile His Ile Phe Ser Phe Thr Gly Glu Glu Met Ala Thr Lys Ala Asp
145 150 155 160
Tyr Thr Leu Asp Glu Glu Ser Arg Ala Arg Ile Lys Thr Arg Leu Phe
165 170 175
Thr Ile Arg Gln Glu Met Ala Ser Arg Gly Leu Trp Asp Ser Phe His
180 185 190
Gln Ser Glu Arg Gly Glu Glu Thr Ile Glu Glu Arg Phe Glu Ile Thr
195 200 205
Gly Thr Met Arg Arg Leu Ala Asp Gln Ser Leu Pro Pro Asn Phe Ser
210 215 220
Cys Leu Glu Asn Phe Arg Ala Tyr Val Asp Gly Phe Glu Pro Asn Gly
225 230 235 240
Tyr Ile Glu Gly Lys Leu Ser Gln Met Ser Lys Glu Val Asn Ala Lys
245 250 255
Ile Glu Pro Phe Leu Lys Thr Thr Pro Arg Pro Ile Arg Leu Pro Asp
260 265 270
Gly Pro Pro Cys Ser Gln Arg Ser Lys Phe Leu Leu Met Asp Ala Leu
275 280 285
Lys Leu Ser Ile Glu Asp Pro Ser His Glu Gly Glu Gly Ile Pro Leu
290 295 300
Tyr Asp Ala Ile Lys Cys Met Arg Thr Phe Phe Gly Trp Lys Glu Pro
305 310 315 320
Tyr Val Val Lys Pro His Glu Lys Gly Ile Asn Pro Asn Tyr Leu Leu
325 330 335
Ser Trp Lys Gln Val Leu Ala Glu Leu Gln Asp Ile Glu Asn Glu Glu
340 345 350

09573569 Sequence Listing.txt

Lys Ile Pro Arg Thr Lys Asn Met Lys Lys Thr Ser Gln Leu Lys Trp
 355 360 365
 Ala Leu Gly Glu Asn Met Ala Pro Glu Lys Val Asp Phe Asp Asp Cys
 370 375 380
 Arg Asp Val Ser Asp Leu Lys Gln Tyr Asp Ser Asp Glu Pro Glu Leu
 385 390 395 400
 Arg Ser Leu Ser Ser Trp Ile Gln Asn Glu Phe Asn Lys Ala Cys Glu
 405 410 415
 Leu Thr Asp Ser Ile Trp Ile Glu Leu Asp Glu Ile Gly Glu Asp Val
 420 425 430
 Ala Pro Ile Glu His Ile Ala Ser Met Arg Arg Asn Tyr Phe Thr Ala
 435 440 445
 Glu Val Ser His Cys Arg Ala Thr Glu Tyr Ile Met Lys Gly Val Tyr
 450 455 460
 Ile Asn Thr Ala Leu Leu Asn Ala Ser Cys Ala Ala Met Asp Asp Phe
 465 470 475 480
 Gln Leu Ile Pro Met Ile Ser Lys Cys Arg Thr Lys Glu Gly Arg Arg
 485 490 495
 Lys Thr Asn Leu Tyr Gly Phe Ile Ile Lys Gly Arg Ser His Leu Arg
 500 505 510
 Asn Asp Thr Asp Val Val Asn Phe Val Ser Met Glu Phe Ser Leu Thr
 515 520 525
 Asp Pro Arg Leu Glu Pro His Lys Trp Glu Lys Tyr Cys Val Leu Glu
 530 535 540
 Ile Gly Asp Met Leu Leu Arg Ser Ala Ile Gly Gln Val Ser Arg Pro
 545 550 555 560
 Met Phe Leu Tyr Val Arg Thr Asn Gly Thr Ser Lys Ile Lys Met Lys
 565 570 575
 Trp Gly Met Glu Met Arg Arg Cys Leu Leu Gln Ser Leu Gln Gln Ile
 580 585 590
 Glu Ser Met Ile Glu Ala Glu Ser Ser Val Lys Glu Lys Asp Met Thr
 595 600 605
 Lys Glu Phe Phe Glu Asn Lys Ser Glu Thr Trp Pro Ile Gly Glu Ser
 610 615 620
 Pro Lys Gly Val Glu Glu Gly Ser Ile Gly Lys Val Cys Arg Thr Leu
 625 630 635 640
 Leu Ala Lys Ser Val Phe Asn Ser Leu Tyr Ala Ser Pro Gln Leu Glu
 645 650 655
 Gly Phe Ser Ala Glu Ser Arg Lys Leu Leu Leu Val Val Gln Ala Leu
 660 665 670
 Arg Asp Asn Leu Glu Pro Gly Thr Phe Asp Leu Gly Gly Leu Tyr Glu
 675 680 685

09573569 Sequence Listing.txt

Ala Ile Glu Glu Cys Leu Ile Asn Asp Pro Trp Val Leu Leu Asn Ala
690 695 700

Ser Trp Phe Asn Ser Phe Leu Thr His Ala Pro Arg
705 710 715

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold adapted "Master Strain" A/AA/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PB1

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(123, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(486, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1195, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(1276, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain; a in wt2(3); g
in 1988 reported ca vaccine strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1395, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1766, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict

09573569 Sequence Listing.txt

(B) LOCATION: replace(2005, "a")
 (D) OTHER INFORMATION: /note= "a in ca "master" strain and in wt2(3)"
 /citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict
 (B) LOCATION: replace(2019, "u")
 (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3)"
 /citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 25..2295
 (D) OTHER INFORMATION: /product= "polymerase basic 1"
 /gene= "PB1"
 /note= "polymerase basic 1"
 /citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
 Maassab, H F
 Webster, R G
 (B) TITLE: Molecular and biological changes in the cold
 adapted master strain A/AA/6/60 (H2N2) influenza
 virus
 (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
 (G) DATE: 1993
 (K) RELEVANT RESIDUES IN SEQ ID NO:13: FROM 1 TO 2341

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
 Kitame, F
 Kendal, A P
 Maassab, H F
 Naeve, C
 (B) TITLE: Identification of sequence changes in the
 cold-adapted live attenuated influenza vaccine
 strain
 (C) JOURNAL: Virology
 (D) VOLUME: 167
 (F) PAGES: 554-567
 (G) DATE: 1988
 (K) RELEVANT RESIDUES IN SEQ ID NO:13: FROM 1 TO 2341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCGAAAGCA GGCAAACCAU UUGA AUG GAU GUC AAU CCG ACC UUA CUU UUC	51
Met Asp Val Asn Pro Thr Leu Leu Phe	
1 5	
UUG AAA GUU CCA GCG CAA AAU GCC AUA AGU ACU ACA UUC CCU UAU ACU	99
Leu Lys Val Pro Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr	
10 15 20 25	
GGA GAU CCU CCA UAC AGC CAU GGG ACA GGA ACA GGA UAC ACC AUG GAC	147
Gly Asp Pro Pro Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp	
30 35 40	
ACA GUC AAC AGA ACA CAU CAA UAU UCA GAA AAG GGG AAG UGG ACA ACA	195
Thr Val Asn Arg Thr His Gln Tyr Ser Glu Lys Gly Lys Trp Thr Thr	
45 50 55	

09573569 Sequence Listing.txt

AAC Asn	ACG Thr	GAA Glu 60	ACU Thr	GGA Gly	GCG Ala	CAC His	CAA Gln 65	CUU Leu	AAC Asn	CCA Pro	AUU Ile	GAU Asp 70	GGA Gly	CCA Pro	CUA Leu	243
CCU Pro	GAG Glu 75	GAC Asp	AAU Asn	GAA Glu	CCA Pro	AGU Ser 80	GGA Gly	UAU Tyr	GCA Ala	CAA Gln	ACA Thr 85	GAC Asp	UGC Cys	GUC Val	CUG Leu	291
GAA Glu 90	GCA Ala	AUG Met	GCU Ala	UUC Phe	CUU Leu 95	GAA Glu	GAA Glu	UCC Ser	CAC His	CCA Pro 100	GGA Gly	AUC Ile	UUU Phe	GAA Glu	AAC Asn 105	339
UCG Ser	UGU Cys	CUU Leu	GAA Glu	ACG Thr 110	AUG Met	GAA Glu	GUU Val	AUU Ile	CAA Gln 115	CAA Gln	ACA Thr	AGA Arg	GUG Val	GAC Asp 120	AAA Lys	387
CUG Leu	ACC Thr	CAA Gln	GGU Gly 125	CGU Arg	CAG Gln	ACC Thr	UAU Tyr	GAU Asp 130	UGG Trp	ACA Thr	UUG Leu	AAC Asn	AGA Arg 135	AAU Asn	CAG Gln	435
CCG Pro	GCU Ala 140	GCA Ala	ACU Thr	GCG Ala	CUA Leu	GCC Ala	AAC Asn 145	ACU Thr	AUA Ile	GAG Glu	GUC Val	UUC Phe 150	AGA Arg	UCG Ser	AAU Asn	483
GGU Gly 155	CUG Leu	ACA Thr	GCU Ala	AAU Asn	GAA Glu	UCG Ser 160	GGA Gly	AGG Arg	CUA Leu	AUA Ile	GAU Asp 165	UUC Phe	CUC Leu	AAG Lys	GAU Asp	531
GUG Val 170	AUA Ile	GAA Glu	UCA Ser	AUG Met	GAU Asp 175	AAA Lys	GAG Glu	GAG Glu	AUG Met	GAA Glu 180	AUC Ile	ACA Thr	ACA Thr	CAC His	UUC Phe 185	579
CAA Gln	AGA Arg	AAA Lys	AGA Arg	AGA Arg 190	GUA Val	AGA Arg	GAC Asp	AAC Asn	AUG Met 195	ACC Thr	AAG Lys	AAA Lys	AUG Met	GUC Val 200	ACA Thr	627
CAA Gln	CGA Arg	ACA Thr	AUA Ile 205	GGA Gly	AAG Lys	AAG Lys	AAG Lys	CAA Gln 210	AGA Arg	UUG Leu	AAC Asn	AAG Lys	AGA Arg 215	AGC Ser	UAU Tyr	675
CUA Leu	AUA Ile	AGA Arg 220	GCA Ala	CUG Leu	ACA Thr	UUG Leu	AAC Asn 225	ACA Thr	AUG Met	ACU Thr	AAA Lys	GAU Asp 230	GCA Ala	GAG Glu	AGA Arg	723
GGU Gly 235	AAA Lys	UUA Leu	AAG Lys	AGA Arg	AGA Arg	GCA Ala 240	AUU Ile	GCA Ala	ACA Thr	CCC Pro	GGU Gly 245	AUG Met	CAG Gln	AUC Ile	AGA Arg	771
GGG Gly 250	UUC Phe	GUG Val	UAC Tyr	UUU Phe	GUC Val 255	GAA Glu	ACA Thr	CUA Leu	GCG Ala	AGA Arg 260	AGU Ser	AUU Ile	UGU Cys	GAG Glu	AAG Lys 265	819
CUU Leu	GAA Glu	CAG Gln	UCU Ser	GGG Gly 270	CUU Leu	CCG Pro	GUU Val	GGA Gly	GGU Gly 275	AAU Asn	GAA Glu	AAG Lys	AAG Lys	GCU Ala 280	AAA Lys	867
CUG Leu	GCA Ala	AAU Asn	GUU Val 285	GUG Val	CGA Arg	AAA Lys	AUG Met	AUG Met	ACU Thr 290	AAU Asn	UCA Ser	CAA Gln	GAC Asp 295	ACA Thr	GAG Glu	915
CUC Leu	UCU Ser	UUC Phe 300	ACA Thr	AUU Ile	ACU Thr	GGA Gly	GAC Asp 305	AAU Asn	ACC Thr	AAA Lys	UGG Trp	AAU Asn 310	GAG Glu	AAU Asn	CAA Gln	963

09573569 Sequence Listing.txt

AAU CCU CGG AUG UUC CUG GCG AUG AUA ACA UAC AUC ACA AGA AAU CAA Asn Pro Arg Met Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln 315 320 325	1011
CCU GAA UGG UUU AGA AAC GUC CUG AGC AUC GCA CCU AUA AUG UUC UCA Pro Glu Trp Phe Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser 330 335 340 345	1059
AAU AAA AUG GCA AGA CUA GGG AAA GGA UAC AUG UUC AAA AGC AAG AGC Asn Lys Met Ala Arg Leu Gly Lys Gly Tyr Met Phe Lys Ser Lys Ser 350 355 360	1107
AUG AAG CUC CGA ACA CAA AUA CCA GCA GAA AUG CUA GCA AGU AUU GAC Met Lys Leu Arg Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp 365 370 375	1155
CUG AAA UAC UUU AAU GAA UCA ACA AGA AAG AAA AUC GAG GAA AUA AGG Leu Lys Tyr Phe Asn Glu Ser Thr Arg Lys Lys Ile Glu Glu Ile Arg 380 385 390	1203
CCU CUC CUA AUA GAU GGC ACA GUC UCA UUG AGU CCU GGA AUG AUG AUG Pro Leu Leu Ile Asp Gly Thr Val Ser Leu Ser Pro Gly Met Met Met 395 400 405	1251
GGC AUG UUC AAC AUG CUA AGU ACA GUC UUA GGA GUC UCA AUC CUG AAU Gly Met Phe Asn Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn 410 415 420 425	1299
CUU GGA CAA AAG AAG UAC ACC AAA ACA ACA UAC UGG UGG GAC GGA CUC Leu Gly Gln Lys Lys Tyr Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu 430 435 440	1347
CAA UCC UCU GAU GAC UUC GCC CUC AUA GUG AAU GCA CCA AAU CAU GAU Gln Ser Ser Asp Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Asp 445 450 455	1395
GGA AUA CAA GCA GGG GUG GAU AGA UUC UAC AGA ACC UGC AAG CUA GUC Gly Ile Gln Ala Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val 460 465 470	1443
GGA AUC AAU AUG AGC AAA AAG AAG UCC UAC AUA AAU AGG ACA GGG ACA Gly Ile Asn Met Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr 475 480 485	1491
UUU GAA UUC ACA AGC UUU UUC UAU CGC UAU GGA UUU GUA GCC AAU UUU Phe Glu Phe Thr Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe 490 495 500 505	1539
AGC AUG GAG CUG CCC AGC UUU GGA GUG UCU GGA AUU AAU GAA UCG GCU Ser Met Glu Leu Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala 510 515 520	1587
GAU AUG AGC AUU GGG GUA ACA GUG AUA AAG AAC AAC AUG AUA AAC AAU Asp Met Ser Ile Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn 525 530 535	1635
GAC CUU GGG CCA GCA ACA GCC CAA CUG GCU CUU CAA CUA UUC AUC AAA Asp Leu Gly Pro Ala Thr Ala Gln Leu Ala Leu Gln Leu Phe Ile Lys 540 545 550	1683
GAC UAC AGA UAU ACG UAC CGG UGC CAC AGA GGA GAC ACA CAA AUU CAG Asp Tyr Arg Tyr Thr Arg Cys His Arg Gly Asp Thr Gln Ile Gln 555	1731

09573569 Sequence Listing.txt

555	560	565	
ACA AGG AGA UCA UUC GAG CUA AAG AAG CUG UGG GGG CAA ACC CGC UCA Thr Arg Arg Ser Phe Glu Leu Lys Lys Leu Trp Gly Gln Thr Arg Ser 570 575 580 585			1779
AAG GCA GGA CUU UUG GUU UCG GAU GGA GGA CCA AAC UUA UAC AAU AUC Lys Ala Gly Leu Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile 590 600			1827
CGG AAU CUC CAC AUU CCA GAA GUC UGC UUG AAG UGG GAG CUA AUG GAU Arg Asn Leu His Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp 605 610 615			1875
GAA GAC UAU CAG GGG AGG CUU UGU AAU CCC CUG AAU CCA UUU GUC AGU Glu Asp Tyr Gln Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Ser 620 625 630			1923
CAU AAG GAG AUU GAG UCU GUA AAC AAU GCU GUG GUA AUG CCA GCU CAC His Lys Glu Ile Glu Ser Val Asn Asn Ala Val Val Met Pro Ala His 635 640 645			1971
GGU CCA GCC AAG AGC AUG GAA UAU GAU GCU GUU ACU ACU ACA CAC UCU Gly Pro Ala Lys Ser Met Glu Tyr Asp Ala Val Thr Thr Thr His Ser 650 655 660 665			2019
UGG AUC CCU AAG AGG AAC CGC UCC AUU CUC AAC ACA AGC CAA AGG GGA Trp Ile Pro Lys Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly 670 675 680			2067
AUU CUU GAA GAU GAA CAG AUG UAU CAG AAG UGU UGC AAU CUA UUC GAG Ile Leu Glu Asp Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu 685 690 695			2115
AAA UUC UUC CCU AGC AGU UCG UAC AGG AGA CCA GUU GGA AUU UCC AGC Lys Phe Phe Pro Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser 700 705 710			2163
AUG GUG GAG GCC AUG GUG UCU AGG GCC CGG AUU GAU GCA CGG AUU GAC Met Val Glu Ala Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp 715 720 725			2211
UUC GAG UCU GGA CGG AUU AAG AAA GAG GAG UUC GCU GAG AUC AUG AAG Phe Glu Ser Gly Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys 730 735 740 745			2259
AUC UGU UCC ACC AUU GAA GAG CUC AGA CGG CAA AAA UAGUGAAUUU Ile Cys Ser Thr Ile Glu Glu Leu Arg Arg Gln Lys 750 755			2305
AGCUUGUCCU UCAUGAAAAA AUGCCUUGUU UCUACU			2341

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

09573569 Sequence Listing.txt

Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
1 5 10 15
Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
20 25 30
Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
35 40 45
Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr Gly Ala His
50 55 60
Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65 70 75 80
Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
85 90 95
Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu Thr Met Glu
100 105 110
Val Ile Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
115 120 125
Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
130 135 140
Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
145 150 155 160
Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Ile Glu Ser Met Asp Lys
165 170 175
Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
180 185 190
Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Lys
195 200 205
Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
210 215 220
Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
225 230 235 240
Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
245 250 255
Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
260 265 270
Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
275 280 285
Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
290 295 300
Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
305 310 315 320
Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
325 330 335

09573569 Sequence Listing.txt

Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Lys Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Ser
 370 375 380
 Thr Arg Lys Lys Ile Glu Glu Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Val Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Lys Tyr Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Asp Gly Ile Gln Ala Gly Val Asp
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Leu Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
 565 570 575
 Lys Lys Leu Trp Gly Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
 645 650 655
 Tyr Asp Ala Val Thr Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670

09573569 Sequence Listing.txt

```

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
    675                      680                      685
Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
    690                      695                      700
Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
    705                      710                      715                      720
Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
    725                      730                      735
Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
    740                      745                      750
Leu Arg Arg Gln Lys
    755

```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PB2

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(141, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain; a in wt2(3); g in 1988 reported ca vaccine strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(426, "c")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(714, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3); c in 1988 reported ca vaccine strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(821, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3)"
/citation= ([1][2])

09573569 Sequence Listing.txt

- (ix) FEATURE:
 (A) NAME/KEY: conflict
 (B) LOCATION: replace(963, "g")
 (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3);
 a in 1988 reported ca vaccine strain"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: conflict
 (B) LOCATION: replace(1182, "u")
 (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3)"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: conflict
 (B) LOCATION: replace(1212, "u")
 (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3)"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: conflict
 (B) LOCATION: replace(1353, "g")
 (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3)"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: conflict
 (B) LOCATION: replace(1923, "g")
 (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3)"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: mutation
 (B) LOCATION: replace(1933, "c")
 (D) OTHER INFORMATION: /note= "c in ca "master" strain; u in wt2(3); u
 in 1988 reported ca vaccine strain"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 28..2304
 (D) OTHER INFORMATION: /product= "polymerase basic 2"
 /gene= "PB2"
 /note= "polymerase basic 2"
 /citation= ([1][2])
- (x) PUBLICATION INFORMATION:
 (A) AUTHORS: Herlocher, M L
 Maassab, H F
 Webster, R G
 (B) TITLE: Molecular and biological changes in the cold
 adapted master strain A/AA/6/60 (H2N2) influenza
 virus
 (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
 (G) DATE: 1993
 (K) RELEVANT RESIDUES IN SEQ ID NO:15: FROM 1 TO 2341
- (x) PUBLICATION INFORMATION:
 (A) AUTHORS: Cox, N J
 Kitame, F
 Kendal, A P
 Maassab, H F
 Naeve, C

09573569 Sequence Listing.txt

(B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain, A/Ann Arbor/6/60(H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:15: FROM 1 TO 2341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGCGAAAGCA	GGUCAUUUAU	AUUCAAU	AUG	GAA	AGA	AUA	AAA	GAA	CUA	CGG	51					
	Met	Glu	Arg	Ile	Lys	Glu	Leu	Arg								
	1				5											
AAU	CUG	AUG	UCG	CAG	UCU	CGC	ACU	CGC	GAG	AUA	CUA	ACA	AAA	ACC	ACA	99
Asn	Leu	Met	Ser	Gln	Ser	Arg	Thr	Arg	Glu	Ile	Leu	Thr	Lys	Thr	Thr	
	10					15					20					
GUG	GAC	CAU	AUG	GCC	AUA	AUU	AAG	AAG	UAC	ACA	UCA	GGG	AGG	CAG	GAA	147
Val	Asp	His	Met	Ala	Ile	Ile	Lys	Lys	Tyr	Thr	Ser	Gly	Arg	Gln	Glu	
	25				30					35					40	
AAG	AAC	CCG	UCA	CUU	AGG	AUG	AAA	UGG	AUG	AUG	GCA	AUG	AAA	UAU	CCG	195
Lys	Asn	Pro	Ser	Leu	Arg	Met	Lys	Trp	Met	Met	Ala	Met	Lys	Tyr	Pro	
				45					50					55		
AUU	ACA	GCC	GAC	AAG	AGG	AUA	ACA	GAA	AUG	AUU	CCU	GAG	AGA	AAU	GAG	243
Ile	Thr	Ala	Asp	Lys	Arg	Ile	Thr	Glu	Met	Ile	Pro	Glu	Arg	Asn	Glu	
			60					65					70			
CAA	GGG	CAA	ACU	CUA	UGG	AGU	AAA	AUG	AGU	GAU	GCC	GGA	UCG	GAU	CGU	291
Gln	Gly	Gln	Thr	Leu	Trp	Ser	Lys	Met	Ser	Asp	Ala	Gly	Ser	Asp	Arg	
		75					80					85				
GUG	AUG	GUA	UCA	CCU	CUG	GCU	GUG	ACA	UGG	UGG	AAU	AGA	AAU	GGA	CCA	339
Val	Met	Val	Ser	Pro	Leu	Ala	Val	Thr	Trp	Trp	Asn	Arg	Asn	Gly	Pro	
	90					95					100					
AUG	ACA	AGU	ACG	GUU	CAU	UAU	CCA	AAA	AUC	UAC	AAA	ACU	UAU	UUU	GAG	387
Met	Thr	Ser	Thr	Val	His	Tyr	Pro	Lys	Ile	Tyr	Lys	Thr	Tyr	Phe	Glu	
	105				110					115					120	
AAA	GUC	GAA	AGG	UUA	AAA	CAU	GGA	ACC	UUU	GGC	CCU	GUC	CAU	UUU	AGA	435
Lys	Val	Glu	Arg	Leu	Lys	His	Gly	Thr	Phe	Gly	Pro	Val	His	Phe	Arg	
				125					130					135		
AAC	CAA	GUC	AAA	AUA	CGC	CGA	AGA	GUU	GAC	AUA	AAU	CCU	GGU	CAU	GCA	483
Asn	Gln	Val	Lys	Ile	Arg	Arg	Arg	Val	Asp	Ile	Asn	Pro	Gly	His	Ala	
			140					145					150			
GAC	CUC	AGU	GCC	AAG	GAG	GCA	CAG	GAU	GUA	AUC	AUG	GAA	GUU	GUU	UUC	531
Asp	Leu	Ser	Ala	Lys	Glu	Ala	Gln	Asp	Val	Ile	Met	Glu	Val	Val	Phe	
		155					160					165				
CCU	AAC	GAA	GUG	GGG	GCC	AGG	AUA	CUA	ACG	UCG	GAA	UCG	CAA	UUA	ACA	579
Pro	Asn	Glu	Val	Gly	Ala	Arg	Ile	Leu	Thr	Ser	Glu	Ser	Gln	Leu	Thr	
	170					175					180					
AUA	ACC	AAA	GAG	AAA	AAA	GAA	GAA	CUC	CAG	GAU	UGC	AAA	AUU	UCA	CCU	627
Ile	Thr	Lys	Glu	Lys	Lys	Glu	Glu	Leu	Gln	Asp	Cys	Lys	Ile	Ser	Pro	
	185				190					195					200	

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UUG Leu	AUG Met	GUU Val	GCG Ala	UAC Tyr 205	AUG Met	UUA Leu	GAG Glu	AGA Arg	GAA Glu 210	CUU Leu	GUC Val	CGA Arg	AAA Lys	ACG Thr 215	AGA Arg	675
UUU Phe	CUC Leu	CCA Pro	GUU Val 220	GCU Ala	GGU Gly	GGA Gly	ACA Thr	AGC Ser 225	AGU Ser	GUG Val	UAC Tyr	AUU Ile	GAA Glu 230	GUG Val	UUG Leu	723
CAC His	UUG Leu	ACU Thr 235	CAA Gln	GGA Gly	ACA Thr	UGC Cys	UGG Trp 240	GAA Glu	CAG Gln	AUG Met	UAC Tyr	ACU Thr 245	CCA Pro	GGU Gly	GGA Gly	771
GAA Glu	GUG Val 250	AGG Arg	AAU Asn	GAU Asp	GAU Asp	GUU Val 255	GAU Asp	CAA Gln	AGU Ser	CUA Leu	AUU Ile 260	AUU Ile	GCA Ala	GCC Ala	AGG Arg	819
AGC Ser 265	AUA Ile	GUG Val	AGA Arg	AGA Arg	GCA Ala 270	GCA Ala	GUA Val	UCA Ser	GCA Ala	GAU Asp 275	CCA Pro	CUA Leu	GCA Ala	UCU Ser	UUA Leu 280	867
UUG Leu	GAG Glu	AUG Met	UGC Cys	CAC His 285	AGC Ser	ACA Thr	CAG Gln	AUU Ile	GGC Gly 290	GGG Gly	ACA Thr	AGG Arg	AUG Met	GUG Val 295	GAC Asp	915
AUU Ile	CUU Leu	AGG Arg	CAG Gln 300	AAC Asn	CCA Pro	ACG Thr	GAA Glu	GAG Glu 305	CAA Gln	GCU Ala	GUG Val	GAA Glu	AUA Ile 310	UGC Cys	AAG Lys	963
GCU Ala	GCA Ala	AUG Met 315	GGA Gly	CUG Leu	AGG Arg	AUC Ile	AGC Ser 320	UCA Ser	UCC Ser	UUC Phe	AGU Ser	UUU Phe 325	GGC Gly	GGG Gly	UUC Phe	1011
ACA Thr 330	UUU Phe	AAG Lys	AGA Arg	ACA Thr	AGC Ser	GGA Gly 335	UCA Ser	UCA Ser	GUC Val	AAG Lys	AGA Arg 340	GAG Glu	GAA Glu	GAA Glu	GUG Val	1059
CUU Leu 345	ACG Thr	GGC Gly	AAU Asn	CUU Leu	CAA Gln 350	ACA Thr	UUG Leu	AAA Lys	AUA Ile	AGG Arg 355	GUG Val	CAU His	GAG Glu	GGA Gly	UAC Tyr 360	1107
GAG Glu	GAG Glu	UUC Phe	ACA Thr	AUG Met 365	GUU Val	GGG Gly	AAA Lys	AGG Arg	GCA Ala 370	ACA Thr	GCU Ala	AUA Ile	CUC Leu	AGA Arg 375	AAA Lys	1155
GCA Ala	ACC Thr	AGG Arg	AGA Arg 380	UUG Leu	AUU Ile	CAG Gln	CUG Leu	AUU Ile 385	GUG Val	AGU Ser	GGA Gly	AGA Arg	GAC Asp 390	GAA Glu	CAG Gln	1203
UCG Ser	AUA Ile	GCU Ala 395	GAA Glu	GCA Ala	AUA Ile	AUU Ile	GUG Val 400	GCC Ala	AUG Met	GUA Val	UUU Phe	UCA Ser 405	CAA Gln	GAA Glu	GAU Asp	1251
UGU Cys	AUG Met 410	AUA Ile	AAA Lys	GCA Ala	GUU Val	AGA Arg 415	GGU Gly	GAU Asp	CUG Leu	AAU Asn	UUC Phe 420	GUU Val	AAU Asn	AGG Arg	GCA Ala	1299
AAU Asn 425	CAG Gln	CGA Arg	UUG Leu	AAU Asn	CCC Pro 430	AUG Met	CAU His	CAA Gln	CUU Leu	UUA Leu 435	AGA Arg	CAU His	UUU Phe	CAG Gln	AAG Lys 440	1347
GAU Asp	GCG Ala	AAA Lys	GUG Val	CUU Leu	UUU Phe	CAA Gln	AAU Asn	UGG Trp	GGA Gly	AUU Ile	GAA Glu	CAU His	AUC Ile	GAC Asp	AAU Asn	1395

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445															450	455															
GUG	AUG	GGA	AUG	AUU	GGG	GUA	UUA	CCA	GAC	AUG	ACU	CCA	AGC	ACA	GAG	1443															
Val	Met	Gly	Met	Ile	Gly	Val	Leu	Pro	Asp	Met	Thr	Pro	Ser	Thr	Glu																
			460					465					470																		
AUG	UCA	AUG	AGA	GGG	GUA	AGA	GUC	AGC	AAA	AUG	GGC	GUA	GAU	GAA	UAC	1491															
Met	Ser	Met	Arg	Gly	Val	Arg	Val	Ser	Lys	Met	Gly	Val	Asp	Glu	Tyr																
		475					480					485																			
UCC	AGC	GCG	GAG	AGA	GUA	GUG	GUG	AGC	AUU	GAC	CGG	UUU	UUG	AGA	GUU	1539															
Ser	Ser	Ala	Glu	Arg	Val	Val	Val	Ser	Ile	Asp	Arg	Phe	Leu	Arg	Val																
	490					495					500																				
CGA	GAC	CAA	CGA	GGA	AAU	GUA	CUA	CUA	UCU	CCU	GAG	GAG	GUC	AGU	GAA	1587															
Arg	Asp	Gln	Arg	Gly	Asn	Val	Leu	Leu	Ser	Pro	Glu	Glu	Val	Ser	Glu																
					510					515					520																
ACA	CAG	GGA	ACA	GAG	AAA	CUG	ACA	AUA	ACU	UAC	UCA	UCG	UCA	AUG	AUG	1635															
Thr	Gln	Gly	Thr	Glu	Lys	Leu	Thr	Ile	Thr	Tyr	Ser	Ser	Ser	Met	Met																
				525					530					535																	
UGG	GAG	AUU	AAU	GGC	CCU	GAG	UCA	GUG	UUG	GUC	AAU	ACC	UAU	CAG	UGG	1683															
Trp	Glu	Ile	Asn	Gly	Pro	Glu	Ser	Val	Leu	Val	Asn	Thr	Tyr	Gln	Trp																
			540					545					550																		
AUC	AUC	AGA	AAC	UGG	GAA	ACU	GUU	AAA	AUU	CAG	UGG	UCU	CAG	AAU	CCU	1731															
Ile	Ile	Arg	Asn	Trp	Glu	Thr	Val	Lys	Ile	Gln	Trp	Ser	Gln	Asn	Pro																
		555					560					565																			
ACA	AUG	CUA	UAC	AAU	AAA	AUG	GAA	UUU	GAG	CCA	UUU	CAG	UCU	UUA	GUU	1779															
Thr	Met	Leu	Tyr	Asn	Lys	Met	Glu	Phe	Glu	Pro	Phe	Gln	Ser	Leu	Val																
	570					575					580																				
CCU	AAG	GCC	AUU	AGA	GGC	CAA	UAC	AGU	GGG	UUU	GUU	AGG	ACU	CUA	UUC	1827															
Pro	Lys	Ala	Ile	Arg	Gly	Gln	Tyr	Ser	Gly	Phe	Val	Arg	Thr	Leu	Phe																
					590				595						600																
CAA	CAA	AUG	AGG	GAU	GUA	CUU	GGG	ACA	UUU	GAU	ACC	ACC	CAG	AUA	AUA	1875															
Gln	Gln	Met	Arg	Asp	Val	Leu	Gly	Thr	Phe	Asp	Thr	Thr	Gln	Ile	Ile																
				605					610					615																	
AAA	CUU	CUU	CCC	UUU	GCA	GCC	GCC	CCA	CCA	AAG	CAA	AGU	AGA	AUG	CAG	1923															
Lys	Leu	Leu	Pro	Phe	Ala	Ala	Ala	Pro	Pro	Lys	Gln	Ser	Arg	Met	Gln																
			620					625					630																		
UUC	UCU	UCA	CUG	ACU	GUG	AAU	GUG	AGG	GGA	UCA	GGA	AUG	AGA	AUA	CUU	1971															
Phe	Ser	Ser	Leu	Thr	Val	Asn	Val	Arg	Gly	Ser	Gly	Met	Arg	Ile	Leu																
		635					640					645																			
GUA	AGG	GGC	AAU	UCU	CCU	AUA	UUC	AAC	UAC	AAC	AAG	ACC	ACU	AAG	AGA	2019															
Val	Arg	Gly	Asn	Ser	Pro	Ile	Phe	Asn	Tyr	Asn	Lys	Thr	Thr	Lys	Arg																
	650					655					660																				
CUA	ACA	AUU	CUC	GGA	AAG	GAU	GCU	GGC	ACU	UUA	ACU	GAA	GAC	CCA	GAU	2067															
Leu	Thr	Ile	Leu	Gly	Lys	Asp	Ala	Gly	Thr	Leu	Thr	Glu	Asp	Pro	Asp																
					670					675					680																
GAA	GGC	ACA	UCU	GGA	GUG	GAG	UCC	GCU	GUU	CUG	AGA	GGA	UUC	CUC	AUU	2115															
Glu	Gly	Thr	Ser	Gly	Val	Glu	Ser	Ala	Val	Leu	Arg	Gly	Phe	Leu	Ile																
				685					690					695																	
CUG	GGC	AAA	GAA	GAU	AGG	AGA	UAU	GGA	CCA	GCA	UUA	AGC	AUC	AAU	GAA	2163															

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Leu	Gly	Lys	Glu	Asp	Arg	Arg	Tyr	Gly	Pro	Ala	Leu	Ser	Ile	Asn	Glu		
			700					705					710				
CUG	AGU	AAC	CUU	GCG	AAA	GGA	GAA	AAG	GCU	AAU	GUA	CUA	AUU	GGG	CAA	2211	
Leu	Ser	Asn	Leu	Ala	Lys	Gly	Glu	Lys	Ala	Asn	Val	Leu	Ile	Gly	Gln		
		715					720					725					
GGA	GAC	GUG	GUG	UUG	GUA	AUG	AAA	CGA	AAA	CGG	AAC	UCU	AGC	AUA	CUU	2259	
Gly	Asp	Val	Val	Leu	Val	Met	Lys	Arg	Lys	Arg	Asn	Ser	Ser	Ile	Leu		
		730				735					740						
ACU	GAC	AGC	CAG	ACA	GCG	ACC	AAA	AGG	AUU	CGG	AUG	GCC	AUC	AAU		2304	
Thr	Asp	Ser	Gln	Thr	Ala	Thr	Lys	Arg	Ile	Arg	Met	Ala	Ile	Asn			
					750					755							
UAAUGUUGAA	UAGUUUAAAA	ACGACCUUGU	UUCUACU													2341	

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Glu	Arg	Ile	Lys	Glu	Leu	Arg	Asn	Leu	Met	Ser	Gln	Ser	Arg	Thr		
1				5					10					15			
Arg	Glu	Ile	Leu	Thr	Lys	Thr	Thr	Val	Asp	His	Met	Ala	Ile	Ile	Lys		
			20					25					30				
Lys	Tyr	Thr	Ser	Gly	Arg	Gln	Glu	Lys	Asn	Pro	Ser	Leu	Arg	Met	Lys		
		35					40					45					
Trp	Met	Met	Ala	Met	Lys	Tyr	Pro	Ile	Thr	Ala	Asp	Lys	Arg	Ile	Thr		
	50					55					60						
Glu	Met	Ile	Pro	Glu	Arg	Asn	Glu	Gln	Gly	Gln	Thr	Leu	Trp	Ser	Lys		
	65				70				75						80		
Met	Ser	Asp	Ala	Gly	Ser	Asp	Arg	Val	Met	Val	Ser	Pro	Leu	Ala	Val		
				85					90					95			
Thr	Trp	Trp	Asn	Arg	Asn	Gly	Pro	Met	Thr	Ser	Thr	Val	His	Tyr	Pro		
			100					105					110				
Lys	Ile	Tyr	Lys	Thr	Tyr	Phe	Glu	Lys	Val	Glu	Arg	Leu	Lys	His	Gly		
		115					120					125					
Thr	Phe	Gly	Pro	Val	His	Phe	Arg	Asn	Gln	Val	Lys	Ile	Arg	Arg	Arg		
	130					135					140						
Val	Asp	Ile	Asn	Pro	Gly	His	Ala	Asp	Leu	Ser	Ala	Lys	Glu	Ala	Gln		
	145				150					155					160		
Asp	Val	Ile	Met	Glu	Val	Val	Phe	Pro	Asn	Glu	Val	Gly	Ala	Arg	Ile		
			165						170					175			
Leu	Thr	Ser	Glu	Ser	Gln	Leu	Thr	Ile	Thr	Lys	Glu	Lys	Lys	Glu	Glu		

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180							185			190						
Leu	Gln	Asp	Cys	Lys	Ile	Ser	Pro	Leu	Met	Val	Ala	Tyr	Met	Leu	Glu	
		195					200					205				
Arg	Glu	Leu	Val	Arg	Lys	Thr	Arg	Phe	Leu	Pro	Val	Ala	Gly	Gly	Thr	
	210					215					220					
Ser	Ser	Val	Tyr	Ile	Glu	Val	Leu	His	Leu	Thr	Gln	Gly	Thr	Cys	Trp	
225					230					235					240	
Glu	Gln	Met	Tyr	Thr	Pro	Gly	Gly	Glu	Val	Arg	Asn	Asp	Asp	Val	Asp	
				245					250					255		
Gln	Ser	Leu	Ile	Ile	Ala	Ala	Arg	Ser	Ile	Val	Arg	Arg	Ala	Ala	Val	
			260					265					270			
Ser	Ala	Asp	Pro	Leu	Ala	Ser	Leu	Leu	Glu	Met	Cys	His	Ser	Thr	Gln	
		275					280					285				
Ile	Gly	Gly	Thr	Arg	Met	Val	Asp	Ile	Leu	Arg	Gln	Asn	Pro	Thr	Glu	
	290					295					300					
Glu	Gln	Ala	Val	Glu	Ile	Cys	Lys	Ala	Ala	Met	Gly	Leu	Arg	Ile	Ser	
305					310					315					320	
Ser	Ser	Phe	Ser	Phe	Gly	Gly	Phe	Thr	Phe	Lys	Arg	Thr	Ser	Gly	Ser	
				325					330					335		
Ser	Val	Lys	Arg	Glu	Glu	Glu	Val	Leu	Thr	Gly	Asn	Leu	Gln	Thr	Leu	
			340					345				350				
Lys	Ile	Arg	Val	His	Glu	Gly	Tyr	Glu	Glu	Phe	Thr	Met	Val	Gly	Lys	
		355					360					365				
Arg	Ala	Thr	Ala	Ile	Leu	Arg	Lys	Ala	Thr	Arg	Arg	Leu	Ile	Gln	Leu	
		370				375					380					
Ile	Val	Ser	Gly	Arg	Asp	Glu	Gln	Ser	Ile	Ala	Glu	Ala	Ile	Ile	Val	
385					390					395					400	
Ala	Met	Val	Phe	Ser	Gln	Glu	Asp	Cys	Met	Ile	Lys	Ala	Val	Arg	Gly	
				405					410					415		
Asp	Leu	Asn	Phe	Val	Asn	Arg	Ala	Asn	Gln	Arg	Leu	Asn	Pro	Met	His	
			420					425					430			
Gln	Leu	Leu	Arg	His	Phe	Gln	Lys	Asp	Ala	Lys	Val	Leu	Phe	Gln	Asn	
		435					440					445				
Trp	Gly	Ile	Glu	His	Ile	Asp	Asn	Val	Met	Gly	Met	Ile	Gly	Val	Leu	
	450					455					460					
Pro	Asp	Met	Thr	Pro	Ser	Thr	Glu	Met	Ser	Met	Arg	Gly	Val	Arg	Val	
465					470					475					480	
Ser	Lys	Met	Gly	Val	Asp	Glu	Tyr	Ser	Ser	Ala	Glu	Arg	Val	Val	Val	
				485				490						495		
Ser	Ile	Asp	Arg	Phe	Leu	Arg	Val	Arg	Asp	Gln	Arg	Gly	Asn	Val	Leu	
			500					505					510			
Leu	Ser	Pro	Glu	Glu	Val	Ser	Glu	Thr	Gln	Gly	Thr	Glu	Lys	Leu	Thr	

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515
 Ile Thr Tyr Ser Ser Ser Met Met Trp Glu Ile Asn Gly Pro Glu Ser
 530 535 540
 Val Leu Val Asn Thr Tyr Gln Trp Ile Ile Arg Asn Trp Glu Thr Val
 545 550 555 560
 Lys Ile Gln Trp Ser Gln Asn Pro Thr Met Leu Tyr Asn Lys Met Glu
 565 570 575
 Phe Glu Pro Phe Gln Ser Leu Val Pro Lys Ala Ile Arg Gly Gln Tyr
 580 585 590
 Ser Gly Phe Val Arg Thr Leu Phe Gln Gln Met Arg Asp Val Leu Gly
 595 600 605
 Thr Phe Asp Thr Thr Gln Ile Ile Lys Leu Leu Pro Phe Ala Ala Ala
 610 615 620
 Pro Pro Lys Gln Ser Arg Met Gln Phe Ser Ser Leu Thr Val Asn Val
 625 630 635 640
 Arg Gly Ser Gly Met Arg Ile Leu Val Arg Gly Asn Ser Pro Ile Phe
 645 650 655
 Asn Tyr Asn Lys Thr Thr Lys Arg Leu Thr Ile Leu Gly Lys Asp Ala
 660 665 670
 Gly Thr Leu Thr Glu Asp Pro Asp Glu Gly Thr Ser Gly Val Glu Ser
 675 680 685
 Ala Val Leu Arg Gly Phe Leu Ile Leu Gly Lys Glu Asp Arg Arg Tyr
 690 695 700
 Gly Pro Ala Leu Ser Ile Asn Glu Leu Ser Asn Leu Ala Lys Gly Glu
 705 710 715 720
 Lys Ala Asn Val Leu Ile Gly Gln Gly Asp Val Val Leu Val Met Lys
 725 730 735
 Arg Lys Arg Asn Ser Ser Ile Leu Thr Asp Ser Gln Thr Ala Thr Lys
 740 745 750
 Arg Ile Arg Met Ala Ile Asn
 755

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

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(B) CLONE: HA

(ix) FEATURE:

(A) NAME/KEY: mutation
(B) LOCATION: replace(144, "u")
(D) OTHER INFORMATION: /gene= "HA"
/note= "u in ca "master" strain; a in w2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: mutation
(B) LOCATION: replace(455, "a")
(D) OTHER INFORMATION: /gene= "HA"
/note= "a in ca "master" strain; g in wt2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: mutation
(B) LOCATION: replace(729, "c")
(D) OTHER INFORMATION: /gene= "HA"
/note= "c in ca "master" strain; a in wt2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 44..1729
(D) OTHER INFORMATION: /product= "hemagglutinin"
/gene= "HA"
/note= "hemagglutinin protein"
/citation= ([1])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
(B) TITLE: Molecular and biological changes in the cold
adapted master strain A/AA/6/60 (H2N2) influenza
virus
(C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
(G) DATE: 1993
(K) RELEVANT RESIDUES IN SEQ ID NO:17: FROM 1 TO 1773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCAAAAGCA GGGGUUAUAC CAUAGACAAC CAAAAGCAAA ACA AUG GCC AUC AUU	55
Met Ala Ile Ile	
1	
UAU CUC AUU CUC CUG UUC ACA GCA GUG AGA GGG GAC AAG AUA UGC AUU	103
Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Asp Lys Ile Cys Ile	
5 10 15 20	
GGA UAC CAU GCC AAU AAU UCC ACA GAG ACG GUC GAC ACA AUU CUA GAG	151
Gly Tyr His Ala Asn Asn Ser Thr Glu Thr Val Asp Thr Ile Leu Glu	
25 30 35	
CGG AAC GUC ACU GUG ACU CAU GCC AAG GAC AUU CUU GAG AAG ACC CAU	199
Arg Asn Val Thr Val Thr His Ala Lys Asp Ile Leu Glu Lys Thr His	
40 45 50	
AAC GGA AAG UUA UGC AAA CUA AAC GGA AUC CCU CCA CUU GAA CUA GGG	247
Asn Gly Lys Leu Cys Lys Leu Asn Gly Ile Pro Pro Leu Glu Leu Gly	

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55	60	65	
GAC UGU AGC AUU GCC GGA UGG CUC CUU GGA AAU CCA GAA UGU GAU AGG Asp Cys Ser Ile Ala Gly Trp Leu Leu Gly Asn Pro Glu Cys Asp Arg	70	75	295
CUU CUA AGU GUG CCA GAA UGG UCC UAU AUA AUG GAG AAA GAA AAC CCG Leu Leu Ser Val Pro Glu Trp Ser Tyr Ile Met Glu Lys Glu Asn Pro	85	90	343
AGA AAC GGU UUG UGU UAU CCA GGC AAC UUC AAU GAU UAU GAA GAA UUG Arg Asn Gly Leu Cys Tyr Pro Gly Asn Phe Asn Asp Tyr Glu Glu Leu	105	110	391
AAA CAU CUC CUC AGC AGC GUG AAA CAU UUC GAG AAA GUA AAG AUU CUG Lys His Leu Leu Ser Ser Val Lys His Phe Glu Lys Val Lys Ile Leu	120	125	439
CCC AAA GAU AGA UGG ACA CAG CAU ACA ACA ACU GGA GGU UCA CAG GCC Pro Lys Asp Arg Trp Thr Gln His Thr Thr Thr Gly Gly Ser Gln Ala	135	140	487
UGC GCG GUG UCU GGU AAU CCA UCA UUC UUC AGG AAC AUG GUC UGG CUG Cys Ala Val Ser Gly Asn Pro Ser Phe Phe Arg Asn Met Val Trp Leu	150	155	535
ACA GAG GAA GGA UCA AAU UAU CCG GUU GCC AAA GGA UCG UAC AAC AAU Thr Glu Glu Gly Ser Asn Tyr Pro Val Ala Lys Gly Ser Tyr Asn Asn	165	170	583
ACA AGC GGA GAA CAA AUG CUA AUA AUU UGG GGG GUG CAC CAU CCC AUU Thr Ser Gly Glu Gln Met Leu Ile Ile Trp Trp Gly Val His His Pro Ile	185	190	631
GAU GAG ACA GAA CAA AGA ACA UUG UAC CAG AAU GUG GGA ACC UAU GUU Asp Glu Thr Glu Gln Arg Thr Leu Tyr Gln Asn Val Gly Thr Tyr Val	200	205	679
UCC GUA GGC ACA UCA ACA UUG AAC AAA AGG UCA ACC CCA GAA AUA GCA Ser Val Gly Thr Ser Thr Leu Asn Lys Arg Ser Thr Pro Glu Ile Ala	215	220	727
ACA AGG CCU AAA GUG AAU GGA CUA GGA AGU AGA AUG GAA UUC UCU UGG Thr Arg Pro Lys Val Asn Gly Leu Gly Ser Arg Met Glu Phe Ser Trp	230	235	775
ACC CUC UUG GAU AUG UGG GAC ACC AUA AAU UUU GAG AGU ACU GGU AAU Thr Leu Leu Asp Met Trp Asp Thr Ile Asn Phe Glu Ser Thr Gly Asn	245	250	823
CUA AUU GCA CCA GAG UAU GGA UUC AAA AUA UCG AAA AGA GGU AGU UCU Leu Ile Ala Pro Glu Tyr Gly Phe Lys Ile Ser Lys Arg Gly Ser Ser	265	270	871
GGG AUC AUG AAA ACA GAA GGA ACA CUU GAG AAC UGU GAG ACC AAA UGC Gly Ile Met Lys Thr Glu Gly Thr Leu Glu Asn Cys Glu Thr Lys Cys	280	285	919
CAA ACU CCU UUG GGA GCA AUA AAU ACA ACA UUG CCU UUU CAC AAU GUC Gln Thr Pro Leu Gly Ala Ile Asn Thr Thr Leu Pro Phe His Asn Val	295	300	967
CAC CCA CUG ACA AUA GGU GAG UGC CCC AAA UAU GUA AAA UCG GAG AAG			1015

09573569 Sequence Listing.txt

His	Pro	Leu	Thr	Ile	Gly	Glu	Cys	Pro	Lys	Tyr	Val	Lys	Ser	Glu	Lys	
310						315					320					
UUG Leu 325	GUC Val	UUA Leu	GCA Ala	ACA Thr	GGA Gly 330	CUA Leu	AGG Arg	AAU Asn	GUU Val	CCC Pro 335	CAG Gln	AUU Ile	GAA Glu	UCA Ser	AGA Arg 340	1063
GGA Gly	UUG Leu	UUU Phe	GGG Gly	GCA Ala 345	AUA Ile	GCU Ala	GGU Gly	UUU Phe	AUA Ile 350	GAA Glu	GGA Gly	GGA Gly	UGG Trp	CAA Gln 355	GGA Gly	1111
AUG Met	GUU Val	GAU Asp	GGU Gly 360	UGG Trp	UAU Tyr	GGA Gly	UAC Tyr	CAU His 365	CAC His	AGC Ser	AAU Asn	GAC Asp	CAG Gln 370	GGA Gly	UCA Ser	1159
GGG Gly	UAU Tyr	GCA Ala 375	GCA Ala	GAC Asp	AAA Lys	GAA Glu	UCC Ser 380	ACU Thr	CAA Gln	AAG Lys	GCA Ala	UUU Phe 385	GAU Asp	GGA Gly	AUC Ile	1207
ACC Thr	AAC Asn 390	AAG Lys	GUA Val	AAU Asn	UCU Ser	GUG Val 395	AUU Ile	GAA Glu	AAG Lys	AUA Ile	AAC Asn 400	ACC Thr	CAA Gln	UUU Phe	GAA Glu	1255
GCU Ala 405	GUU Val	GGG Gly	AAA Lys	GAA Glu	UUC Phe 410	AGU Ser	AAC Asn	UUA Leu	GAG Glu	AGA Arg 415	AGA Arg	CUG Leu	GAG Glu	AAC Asn	UUG Leu 420	1303
AAC Asn	AAA Lys	AAG Lys	AUG Met	GAA Glu 425	GAC Asp	GGG Gly	UUU Phe	CUA Leu	GAU Asp 430	GUG Val	UGG Trp	ACA Thr	UAC Tyr	AAU Asn 435	GCU Ala	1351
GAG Glu	CUU Leu	CUA Leu	GUU Val 440	CUG Leu	AUG Met	GAA Glu	AAU Asn 445	GAG Glu	AGG Arg	ACA Thr	CUU Leu	GAC Asp	UUU Phe 450	CAU His	GAU Asp	1399
UCU Ser	AAU Asn	GUC Val 455	AAG Lys	AAU Asn	CUG Leu	UAU Tyr	GAU Asp 460	AAA Lys	GUC Val	AGA Arg	AUG Met	CAG Gln 465	CUG Leu	AGG Arg	GAC Asp	1447
AAC Asn	GUC Val 470	AAA Lys	GAA Glu	CUA Leu	GGA Gly	AAU Asn 475	GGA Gly	UGU Cys	UUU Phe	GAA Glu	UUU Phe 480	UAU Tyr	CAC His	AAA Lys	UGU Cys	1495
GAU Asp 485	GAU Asp	GAA Glu	UGC Cys	AUG Met	AAU Asn 490	AGU Ser	GUG Val	AAA Lys	AAC Asn	GGG Gly 495	ACA Thr	UAU Tyr	GAU Asp	UAU Tyr	CCC Pro 500	1543
AAG Lys	UAU Tyr	GAA Glu	GAA Glu	GAG Glu 505	UCU Ser	AAA Lys	CUA Leu	AAU Asn	AGA Arg 510	AAU Asn	GAA Glu	AUU Ile	AAA Lys	GGG Gly 515	GUA Val	1591
AAA Lys	UUG Leu	AGC Ser	AGC Ser	AUG Met	GGG Gly	GUU Val	UGU Cys	CGG Arg 525	AUC Ile	CUU Leu	GCC Ala	AUU Ile	UAU Tyr 530	GCU Ala	ACA Thr	1639
GUA Val	GCA Ala	GGU Gly 535	UCU Ser	CUG Leu	UCA Ser	CUG Leu	GCA Ala 540	AUC Ile	AUG Met	AUG Met	GCU Ala	GGG Gly 545	AUC Ile	UCU Ser	UUC Phe	1687
UGG Trp	AUG Met 550	UGC Cys	UCC Ser	AAC Asn	GGG Gly	UCU Ser 555	CUG Leu	CAG Gln	UGC Cys	AGG Arg	AUC Ile 560	UGC Cys	AUA Ile			1729

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 562 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Asp
 1 5 10 15
 Lys Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Thr Val Asp
 20 25 30
 Thr Ile Leu Glu Arg Asn Val Thr Val Thr His Ala Lys Asp Ile Leu
 35 40 45
 Glu Lys Thr His Asn Gly Lys Leu Cys Lys Leu Asn Gly Ile Pro Pro
 50 55 60
 Leu Glu Leu Gly Asp Cys Ser Ile Ala Gly Trp Leu Leu Gly Asn Pro
 65 70 75 80
 Glu Cys Asp Arg Leu Leu Ser Val Pro Glu Trp Ser Tyr Ile Met Glu
 85 90 95
 Lys Glu Asn Pro Arg Asn Gly Leu Cys Tyr Pro Gly Asn Phe Asn Asp
 100 105 110
 Tyr Glu Glu Leu Lys His Leu Leu Ser Ser Val Lys His Phe Glu Lys
 115 120 125
 Val Lys Ile Leu Pro Lys Asp Arg Trp Thr Gln His Thr Thr Thr Gly
 130 135 140
 Gly Ser Gln Ala Cys Ala Val Ser Gly Asn Pro Ser Phe Phe Arg Asn
 145 150 155 160
 Met Val Trp Leu Thr Glu Glu Gly Ser Asn Tyr Pro Val Ala Lys Gly
 165 170 175
 Ser Tyr Asn Asn Thr Ser Gly Glu Gln Met Leu Ile Ile Trp Gly Val
 180 185 190
 His His Pro Ile Asp Glu Thr Glu Gln Arg Thr Leu Tyr Gln Asn Val
 195 200 205
 Gly Thr Tyr Val Ser Val Gly Thr Ser Thr Leu Asn Lys Arg Ser Thr
 210 215 220
 Pro Glu Ile Ala Thr Arg Pro Lys Val Asn Gly Leu Gly Ser Arg Met
 225 230 235 240
 Glu Phe Ser Trp Thr Leu Leu Asp Met Trp Asp Thr Ile Asn Phe Glu
 245 250 255
 Ser Thr Gly Asn Leu Ile Ala Pro Glu Tyr Gly Phe Lys Ile Ser Lys

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260	265	270
Arg Gly Ser Ser Gly Ile Met Lys Thr Glu Gly Thr Leu Glu Asn Cys		
275	280	285
Glu Thr Lys Cys Gln Thr Pro Leu Gly Ala Ile Asn Thr Thr Leu Pro		
290	295	300
Phe His Asn Val His Pro Leu Thr Ile Gly Glu Cys Pro Lys Tyr Val		
305	310	315
Lys Ser Glu Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Val Pro Gln		
325	330	335
Ile Glu Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly		
340	345	350
Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His Ser Asn		
355	360	365
Asp Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala		
370	375	380
Phe Asp Gly Ile Thr Asn Lys Val Asn Ser Val Ile Glu Lys Ile Asn		
385	390	395
Thr Gln Phe Glu Ala Val Gly Lys Glu Phe Ser Asn Leu Glu Arg Arg		
405	410	415
Leu Glu Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp		
420	425	430
Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu		
435	440	445
Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg Met		
450	455	460
Gln Leu Arg Asp Asn Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe		
465	470	475
Tyr His Lys Cys Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly Thr		
485	490	495
Tyr Asp Tyr Pro Lys Tyr Glu Glu Glu Ser Lys Leu Asn Arg Asn Glu		
500	505	510
Ile Lys Gly Val Lys Leu Ser Ser Met Gly Val Cys Arg Ile Leu Ala		
515	520	525
Ile Tyr Ala Thr Val Ala Gly Ser Leu Ser Leu Ala Ile Met Met Ala		
530	535	540
Gly Ile Ser Phe Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile		
545	550	555
560		
Cys Ile		

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1467 base pairs

09573569 Sequence Listing.txt

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Influenza virus
(B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI
(H2N2)

(vii) IMMEDIATE SOURCE:

(B) CLONE: NA

(ix) FEATURE:

(A) NAME/KEY: mutation
(B) LOCATION: replace(394, "u")
(D) OTHER INFORMATION: /product= "Neuraminidase"
/gene= "NA"
/note= "u in ca "master" strain; c in wt2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: mutation
(B) LOCATION: replace(604, "u")
(D) OTHER INFORMATION: /product= "Neuraminidase"
/gene= "NA"
/note= "u in ca "master" strain; a in wt2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 20..1426
(D) OTHER INFORMATION: /product= "neuraminidase"
/gene= "NA"
/note= "neuraminidase protein"
/citation= ([1])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
(B) TITLE: Molecular and biological changes in the cold
adapted master strain A/AA/6/60 (H2N2) Influenza
Virus
(C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
(G) DATE: 1993
(K) RELEVANT RESIDUES IN SEQ ID NO:19: FROM 1 TO 1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCAAAAGCA GGAGUGAAA AUG AAU CCA AAU CAA AAG ACA AUA ACA AUU GGC	52
Met Asn Pro Asn Gln Lys Thr Ile Thr Ile Gly	
1 5 10	
UCU GUC UCU CUC ACC AUC GCA ACA GUA UGC UUC CUC AUG CAG AUU GCC	100
Ser Val Ser Leu Thr Ile Ala Thr Val Cys Phe Leu Met Gln Ile Ala	
15 20 25	
AUC CUG GCA ACU ACU GUG ACA UUG CAC CUU AAG CAA CAU GAG UGC GAC	148
Ile Leu Ala Thr Thr Val Thr Leu His Leu Lys Gln His Glu Cys Asp	
30 35 40	

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UCC Ser	CCC Pro	GCG Ala	AGC Ser	AAC Asn	CAA Gln	GUA Val	AUG Met	CCA Pro	UGU Cys	GAA Glu	CCA Pro	AUA Ile	AUA Ile	AUA Ile	GAA Glu	196
45 50 55																
AGG Arg	AAC Asn	AUA Ile	ACA Thr	GAG Glu	AUA Ile	GUG Val	UAU Tyr	UUG Leu	AAU Asn	AAC Asn	ACC Thr	ACC Thr	AUA Ile	GAG Glu	AAA Lys	244
60 65 70 75																
GAG Glu	AUU Ile	UGC Cys	CCC Pro	GAA Glu	GUA Val	GUG Val	GGA Gly	UAC Tyr	AGA Arg	AAU Asn	UGG Trp	UCA Ser	AAG Lys	CCG Pro	CAA Gln	292
80 85 90																
UGU Cys	CAA Gln	AUU Ile	ACA Thr	GGA Gly	UUU Phe	GCA Ala	CCU Pro	UUU Phe	UCU Ser	AAG Lys	GAC Asp	AAU Asn	UCA Ser	AUC Ile	CGG Arg	340
95 100 105																
CUU Leu	UCU Ser	GCU Ala	GGU Gly	GGG Gly	GAC Asp	AUU Ile	UGG Trp	GUG Val	ACG Thr	AGA Arg	GAA Glu	CCU Pro	UAU Tyr	GUG Val	UCA Ser	388
110 115 120																
UGC Cys	GAU Asp	CCU Pro	GGC Gly	AAG Lys	UGU Cys	UAU Tyr	CAA Gln	UUU Phe	GCA Ala	CUC Leu	GGG Gly	CAG Gln	GGG Gly	ACC Thr	ACA Thr	436
125 130 135																
CUA Leu	GAC Asp	AAC Asn	AAA Lys	CAU His	UCA Ser	AAU Asn	GGC Gly	ACA Thr	AUA Ile	CAU His	GAU Asp	AGA Arg	AUC Ile	CCU Pro	CAU His	484
140 145 150 155																
CGA Arg	ACC Thr	CUA Leu	UUA Leu	AUG Met	AAU Asn	GAG Glu	UUG Leu	GGU Gly	GUU Val	CCA Pro	UUU Phe	CAU His	UUA Leu	GGA Gly	ACC Thr	532
160 165 170																
AAA Lys	CAA Gln	GUG Val	UGU Cys	GCA Ala	GCA Ala	UGG Trp	UCC Ser	AGC Ser	UCA Ser	AGU Ser	UGU Cys	CAC His	GAU Asp	GGA Gly	AAA Lys	580
175 180 185																
GCA Ala	UGG Trp	UUG Leu	CAU His	GUU Val	UGU Cys	GUC Val	ACU Thr	GGG Gly	GAU Asp	GAU Asp	AGA Arg	AAU Asn	GCA Ala	ACU Thr	GCU Ala	628
190 195 200																
AGC Ser	UUC Phe	AUU Ile	UAU Tyr	GAC Asp	GGG Gly	AAG Lys	CUU Leu	GUG Val	GAC Asp	AGU Ser	AUU Ile	GGU Gly	UCA Ser	UGG Trp	UCU Ser	676
205 210 215																
CAA Gln	AAU Asn	GUC Val	CUC Leu	AGG Arg	ACC Thr	CAG Gln	GAG Glu	UCG Ser	GAA Glu	UGC Cys	GUC Val	UGU Cys	AUC Ile	AAU Asn	GGG Gly	724
220 225 230 235																
ACU Thr	UGC Cys	ACA Thr	GUA Val	GUA Val	AUG Met	ACU Thr	GAU Asp	GGA Gly	AGU Ser	GCA Ala	UCA Ser	GGA Gly	AGA Arg	GCU Ala	GAU Asp	772
240 245 250																
ACU Thr	AGA Arg	AUA Ile	CUA Leu	UUC Phe	AUU Ile	AAA Lys	GAG Glu	GGG Gly	AAA Lys	AUU Ile	GUC Val	CAU His	AUU Ile	GGC Gly	CCA Pro	820
255 260 265																
UUG Leu	UCA Ser	GGA Gly	AGU Ser	GCU Ala	CAG Gln	CAU His	GUA Val	GAG Glu	GAG Glu	UGU Cys	UCU Ser	UGU Cys	UAC Tyr	CCU Pro	CGA Arg	868
270 275 280																
UAU Tyr	CCU Pro	GAC Asp	GUC Val	AGA Arg	UGU Cys	AUC Ile	UGC Cys	AGA Arg	GAC Asp	AAC Asn	UGG Trp	AAA Lys	GGC Gly	UCU Ser	AAU Asn	916

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285	290	295	
AGG CCC GUU AUA GAC AUA AAU AUG GAA GAU UAU AGC AUU GAU UCC AGU Arg Pro Val Ile Asp Ile Asn Met Glu Asp Tyr Ser Ile Asp Ser Ser 300 305 310 315			964
UAU GUG UGC UCA GGG CUU GUU GGC GAC ACA CCC AGG AAC GAC GAC AGC Tyr Val Cys Ser Gly Leu Val Gly Asp Thr Pro Arg Asn Asp Asp Ser 320 325 330			1012
UCU AGC AAU AGC AAU UGC AGG GAU CCU AAC AAU GAG AGA GGG AAU CCA Ser Ser Asn Ser Asn Cys Arg Asp Pro Asn Asn Glu Arg Gly Asn Pro 335 340 345			1060
GGA GUG AAA GGC UGG GCC UUU GAC AAU GGA GAU GAU GUA UGG AUG GGA Gly Val Lys Gly Trp Ala Phe Asp Asn Gly Asp Asp Val Trp Met Gly 350 355 360			1108
AGA ACA AUC AGC AAA GAU UUA CGC UCA GGU UAU GAA ACU UUC AAA GUC Arg Thr Ile Ser Lys Asp Leu Arg Ser Gly Tyr Glu Thr Phe Lys Val 365 370 375			1156
AUU GGU GGU UGG UCC ACA CCU AAU UCC AAA UCG CAG GUC AAU AGA CAG Ile Gly Gly Trp Ser Thr Pro Asn Ser Lys Ser Gln Val Asn Arg Gln 380 385 390 395			1204
GUC AUA GUU GAC AAC AAU AAU UGG UCU GGU UAC UCU GGU AUU UUC UCU Val Ile Val Asp Asn Asn Asn Trp Ser Gly Tyr Ser Gly Ile Phe Ser 400 405 410			1252
GUU GAG GGC AAA AGC UGC AUC AAU AGG UGC UUU UAU GUG GAG UUG AUA Val Glu Gly Lys Ser Cys Ile Asn Arg Cys Phe Tyr Val Glu Leu Ile 415 420 425			1300
AGG GGA AGG CCA CAG GAG ACU AGA GUA UGG UGG ACC UCA AAC AGU AUU Arg Gly Arg Pro Gln Glu Thr Arg Val Trp Trp Thr Ser Asn Ser Ile 430 435 440			1348
GUU GUA UUU UGU GGC ACU UCA GGU ACU UAU GGA ACA GGC UCA UGG CCU Val Val Phe Cys Gly Thr Ser Gly Thr Tyr Gly Thr Gly Ser Trp Pro 445 450 455			1396
GAU GGG GCG AAC AUC AAU UUC AUG CCU AUA UAACGUUUCG CAAUUUUAGA Asp Gly Ala Asn Ile Asn Phe Met Pro Ile 460 465			1446
AAAAAACUCC UUGUUUCUAC U			1467

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Asn	Pro	Asn	Gln	Lys	Thr	Ile	Thr	Ile	Gly	Ser	Val	Ser	Leu	Thr
1				5					10					15	

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Ile Ala Thr Val Cys Phe Leu Met Gln Ile Ala Ile Leu Ala Thr Thr
20 25 30
Val Thr Leu His Leu Lys Gln His Glu Cys Asp Ser Pro Ala Ser Asn
35 40 45
Gln Val Met Pro Cys Glu Pro Ile Ile Ile Glu Arg Asn Ile Thr Glu
50 55 60
Ile Val Tyr Leu Asn Asn Thr Thr Ile Glu Lys Glu Ile Cys Pro Glu
65 70 75 80
Val Val Gly Tyr Arg Asn Trp Ser Lys Pro Gln Cys Gln Ile Thr Gly
85 90 95
Phe Ala Pro Phe Ser Lys Asp Asn Ser Ile Arg Leu Ser Ala Gly Gly
100 105 110
Asp Ile Trp Val Thr Arg Glu Pro Tyr Val Ser Cys Asp Pro Gly Lys
115 120 125
Cys Tyr Gln Phe Ala Leu Gly Gln Gly Thr Thr Leu Asp Asn Lys His
130 135 140
Ser Asn Gly Thr Ile His Asp Arg Ile Pro His Arg Thr Leu Leu Met
145 150 155 160
Asn Glu Leu Gly Val Pro Phe His Leu Gly Thr Lys Gln Val Cys Ala
165 170 175
Ala Trp Ser Ser Ser Cys His Asp Gly Lys Ala Trp Leu His Val
180 185 190
Cys Val Thr Gly Asp Asp Arg Asn Ala Thr Ala Ser Phe Ile Tyr Asp
195 200 205
Gly Lys Leu Val Asp Ser Ile Gly Ser Trp Ser Gln Asn Val Leu Arg
210 215 220
Thr Gln Glu Ser Glu Cys Val Cys Ile Asn Gly Thr Cys Thr Val Val
225 230 235 240
Met Thr Asp Gly Ser Ala Ser Gly Arg Ala Asp Thr Arg Ile Leu Phe
245 250 255
Ile Lys Glu Gly Lys Ile Val His Ile Gly Pro Leu Ser Gly Ser Ala
260 265 270
Gln His Val Glu Glu Cys Ser Cys Tyr Pro Arg Tyr Pro Asp Val Arg
275 280 285
Cys Ile Cys Arg Asp Asn Trp Lys Gly Ser Asn Arg Pro Val Ile Asp
290 295 300
Ile Asn Met Glu Asp Tyr Ser Ile Asp Ser Ser Tyr Val Cys Ser Gly
305 310 315 320
Leu Val Gly Asp Thr Pro Arg Asn Asp Asp Ser Ser Ser Asn Ser Asn
325 330 335
Cys Arg Asp Pro Asn Asn Glu Arg Gly Asn Pro Gly Val Lys Gly Trp
340 345 350

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Ala Phe Asp Asn Gly Asp Asp Val Trp Met Gly Arg Thr Ile Ser Lys
 355 360 365
 Asp Leu Arg Ser Gly Tyr Glu Thr Phe Lys Val Ile Gly Gly Trp Ser
 370 375 380
 Thr Pro Asn Ser Lys Ser Gln Val Asn Arg Gln Val Ile Val Asp Asn
 385 390 395 400
 Asn Asn Trp Ser Gly Tyr Ser Gly Ile Phe Ser Val Glu Gly Lys Ser
 405 410 415
 Cys Ile Asn Arg Cys Phe Tyr Val Glu Leu Ile Arg Gly Arg Pro Gln
 420 425 430
 Glu Thr Arg Val Trp Trp Thr Ser Asn Ser Ile Val Val Phe Cys Gly
 435 440 445
 Thr Ser Gly Thr Tyr Gly Thr Gly Ser Trp Pro Asp Gly Ala Asn Ile
 450 455 460
 Asn Phe Met Pro Ile
 465

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 890 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: NS

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 27..56
- (D) OTHER INFORMATION: /product= "nonstructural protein NS2"
 /gene= "NS"
 /note= "nonstructural protein NS2"
 /citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(483, "a")
- (D) OTHER INFORMATION: /note= "a in ca "master" strain and in wt2(3);
 g in 1988 reported wild type E28-32 strain"
 /citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 529..861
- (D) OTHER INFORMATION: /product= "nonstructural protein NS2"
 /gene= "NS"

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/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(813, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3);
a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(27..56, 529..861)
- (D) OTHER INFORMATION: /product= "nonstructural protein
NS2"
/gene= "NS"
/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 27..677
- (D) OTHER INFORMATION: /product= "nonstructural protein
NS1"
/gene= "NS"
/note= "nonstructural protein NS1"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
- (B) TITLE: Molecular and biological changes in the cold
adapted master strain A/AA/6/60 (H2N2) influenza
virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
- (G) DATE: 1993
- (K) RELEVANT RESIDUES IN SEQ ID NO:21: FROM 1 TO 890

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C
- (B) TITLE: Identification of sequence changes in the
cold-adapted live attenuated influenza vaccine
strain, A/Ann Arbor/6/60(H2N2)
- (C) JOURNAL: Virology
- (D) VOLUME: 167
- (F) PAGES: 554-567
- (G) DATE: 1988
- (K) RELEVANT RESIDUES IN SEQ ID NO:21: FROM 1 TO 890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGCAAAAGCA GGGUGACAAA GACAU	AUG GAU CCU AAC ACU GUG UCA AGC UUU	53
	Met Asp Pro Asn Thr Val Ser Ser Phe	
	1 5	
CAG GUA GAU UGC UUC CUU UGG CAU GUC CGC AAA CAA GUU GCA GAC CAA		101

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Gln Val Asp Cys Phe Leu Trp His Val Arg Lys Gln Val Ala Asp Gln	
10 15 20 25	
GAA CUA GGU GAU GCC CCA UUC CUU GAU CGG CUU CGC CGA GAU CAG AAG	149
Glu Leu Gly Asp Ala Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys	
30 35 40	
UCC CUA AGG GGA AGA GGC AGU ACU CUC GGU CUG AAC AUC GAA ACA GCC	197
Ser Leu Arg Gly Arg Gly Ser Thr Leu Gly Leu Asn Ile Glu Thr Ala	
45 50 55	
ACC CGU GUU GGA AAG CAG AUA GUG GAG AGG AUU CUG AAG GAA GAA UCC	245
Thr Arg Val Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser	
60 65 70	
GAU GAG GCA CUU AAA AUG ACC AUG GCC UCC GCA CCU GCU UCG CGA UAC	293
Asp Glu Ala Leu Lys Met Thr Met Ala Ser Ala Pro Ala Ser Arg Tyr	
75 80 85	
CUA ACU GAC AUG ACU AUU GAG GAA AUG UCA AGG GAC UGG UUC AUG CUA	341
Leu Thr Asp Met Thr Ile Glu Glu Met Ser Arg Asp Trp Phe Met Leu	
90 95 100 105	
AUG CCC AAG CAG AAA GUG GCA GGC CCU CUU UGU AUC AGA AUG GAC CAG	389
Met Pro Lys Gln Lys Val Ala Gly Pro Leu Cys Ile Arg Met Asp Gln	
110 115 120	
GCA AUC AUG GAU AAG AAC AUC AUA UUG AAA GCG AAU UUC AGU GUG AUU	437
Ala Ile Met Asp Lys Asn Ile Ile Leu Lys Ala Asn Phe Ser Val Ile	
125 130 135	
UUU GAC CGG CUA GAG ACC CUA AUA UUA CUA AGG GCU UUC ACC GAA ACG	485
Phe Asp Arg Leu Glu Thr Leu Ile Leu Leu Arg Ala Phe Thr Glu Thr	
140 145 150	
GGA GCA AUU GUU GGC GAA AUU UCA CCA UUG CCU UCU CUU CCA GGA CAU	533
Gly Ala Ile Val Gly Glu Ile Ser Pro Leu Pro Ser Leu Pro Gly His	
155 160 165	
ACU AAU GAG GAU GUC AAA AAU GCA AUU GGG GUC CUC AUC GGA GGA CUU	581
Thr Asn Glu Asp Val Lys Asn Ala Ile Gly Val Leu Ile Gly Gly Leu	
170 175 180 185	
GAA UGG AAU GAU AAC ACA GUU CGA GUC UCU AAA ACU CUA CAG AGA UUC	629
Glu Trp Asn Asp Asn Thr Val Arg Val Ser Lys Thr Leu Gln Arg Phe	
190 195 200	
GCU UGG AGA AGC AGU GAU GAG AAU GGG AGA CCU CCA CUC ACU CCA AAA	677
Ala Trp Arg Ser Ser Asp Glu Asn Gly Arg Pro Pro Leu Thr Pro Lys	
205 210 215	
UAGAAACGGA AAAUGGCGAG AACAAUUAGG UCAAAAGUUC GAAGAAUAA GAUGGCUGAU	737
UGAAGAAGUG AGACACAAAU UGAAGAUAAAC AGAGAAUAGU UUUGAGCAAA UAACAUUUAU	797
GCAAGCCUUA CAGCUGCUAU UUGAAGUGGA ACAAGAGAUU AGAACUUUCU CGUUUCAGCU	857
UAUUUAAUGA UAAAAAACAC CCUUGUUUCU ACU	890

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Met Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu Trp
 1          5          10          15
His Val Arg Lys Gln Val Ala Asp Gln Glu Leu Gly Asp Ala Pro Phe
          20          25          30
Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly Arg Gly Ser
          35          40          45
Thr Leu Gly Leu Asn Ile Glu Thr Ala Thr Arg Val Gly Lys Gln Ile
          50          55          60
Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu Ala Leu Lys Met Thr
          65          70          75          80
Met Ala Ser Ala Pro Ala Ser Arg Tyr Leu Thr Asp Met Thr Ile Glu
          85          90          95
Glu Met Ser Arg Asp Trp Phe Met Leu Met Pro Lys Gln Lys Val Ala
          100          105          110
Gly Pro Leu Cys Ile Arg Met Asp Gln Ala Ile Met Asp Lys Asn Ile
          115          120          125
Ile Leu Lys Ala Asn Phe Ser Val Ile Phe Asp Arg Leu Glu Thr Leu
          130          135          140
Ile Leu Leu Arg Ala Phe Thr Glu Thr Gly Ala Ile Val Gly Glu Ile
          145          150          155          160
Ser Pro Leu Pro Ser Leu Pro Gly His Thr Asn Glu Asp Val Lys Asn
          165          170          175
Ala Ile Gly Val Leu Ile Gly Gly Leu Glu Trp Asn Asp Asn Thr Val
          180          185          190
Arg Val Ser Lys Thr Leu Gln Arg Phe Ala Trp Arg Ser Ser Asp Glu
          195          200          205
Asn Gly Arg Pro Pro Leu Thr Pro Lys
          210          215

```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 418 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

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(B) LOCATION: 27..389

(D) OTHER INFORMATION: /product= "Nonstructural protein 2"
/gene= "NS2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCAAAAGCA GGGUGACAAA GACAU	AUG GAU CCU AAC ACU GUG UCA AGC UUU	53
	Met Asp Pro Asn Thr Val Ser Ser Phe	
	1 5	
CAG GAC AUA CUA AUG AGG AUG UCA AAA AUG CAA UUG GGG UCC UCA UCG		101
Gln Asp Ile Leu Met Arg Met Ser Lys Met Gln Leu Gly Ser Ser Ser		
10 15 20 25		
GAG GAC UUG AAU GGA AUG AUA ACA CAG UUC GAG UCU CUA AAA CUC UAC		149
Glu Asp Leu Asn Gly Met Ile Thr Gln Phe Glu Ser Leu Lys Leu Tyr		
	30 35 40	
AGA GAU UCG CUU GGA GAA GCA GUG AUG AGA AUG GGA GAC CUC CAC UCA		197
Arg Asp Ser Leu Gly Glu Ala Val Met Arg Met Gly Asp Leu His Ser		
	45 50 55	
CUC CAA AAU AGA AAC GGA AAA UGG CGA GAA CAA UUA GGU CAA AAG UUC		245
Leu Gln Asn Arg Asn Gly Lys Trp Arg Glu Gln Leu Gly Gln Lys Phe		
	60 65 70	
GAA GAA AUA AGA UGG CUG AUU GAA GAA GUG AGA CAC AAA UUG AAG AUA		293
Glu Glu Ile Arg Trp Leu Ile Glu Glu Val Arg His Lys Leu Lys Ile		
	75 80 85	
ACA GAG AAU AGU UUU GAG CAA AUA ACA UUU AUG CAA GCC UUA CAG CUG		341
Thr Glu Asn Ser Phe Glu Gln Ile Thr Phe Met Gln Ala Leu Gln Leu		
	90 95 100 105	
CUA UUU GAA GUG GAA CAA GAG AUA AGA ACU UUC UCG UUU CAG CUU AUU		389
Leu Phe Glu Val Glu Gln Glu Ile Arg Thr Phe Ser Phe Gln Leu Ile		
	110 115 120	
UAAUGAUAAA AAACACCCUU GUUUCUACU		418

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Asp Pro Asn Thr Val Ser Ser Phe Gln Asp Ile Leu Met Arg Met	
1 5 10 15	
Ser Lys Met Gln Leu Gly Ser Ser Ser Glu Asp Leu Asn Gly Met Ile	
20 25 30	
Thr Gln Phe Glu Ser Leu Lys Leu Tyr Arg Asp Ser Leu Gly Glu Ala	
35 40 45	
Val Met Arg Met Gly Asp Leu His Ser Leu Gln Asn Arg Asn Gly Lys	

50

55

60

Trp Arg Glu Gln Leu Gly Gln Lys Phe Glu Glu Ile Arg Trp Leu Ile
 65 70 75 80

Glu Glu Val Arg His Lys Leu Lys Ile Thr Glu Asn Ser Phe Glu Gln
 85 90 95

Ile Thr Phe Met Gln Ala Leu Gln Leu Leu Phe Glu Val Glu Gln Glu
 100 105 110

Ile Arg Thr Phe Ser Phe Gln Leu Ile
 115 120

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: M

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 26..51
- (D) OTHER INFORMATION: /product= "matrix protein M2"
 /gene= "M"
 /note= "matrix protein M2"
 /citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 740..1004
- (D) OTHER INFORMATION: /product= "matrix protein M2"
 /gene= "M"
 /note= "matrix protein M2"
 /citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(969, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3);
 g in 1988 reported wild type E28-32 strain"
 /citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(26..51, 740..1004)
- (D) OTHER INFORMATION: /product= "matrix protein M2"
 /gene= "M"
 /note= "matrix protein M2"
 /citation= ([1][2])

(ix) FEATURE:

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(A) NAME/KEY: CDS
 (B) LOCATION: 26..781
 (D) OTHER INFORMATION: /product= "matrix protein M1"
 /gene= "M"
 /note= "matrix protein M1"
 /citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
 Maassab, H F
 Webster, R G
 (B) TITLE: Molecular and biological changes in the cold
 adapted master strain A/AA/6/60 (H2N2) influenza
 virus
 (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
 (G) DATE: 1993
 (K) RELEVANT RESIDUES IN SEQ ID NO:25: FROM 1 TO 1027

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
 Kitame, F
 Kendal, A P
 Maassab, H F
 Naeve, C
 (B) TITLE: Identification of sequence changes in the
 cold-adapted live attenuated influenza vaccine
 strain, A/Ann Arbor/6/60(H2N2)
 (C) JOURNAL: Virology
 (D) VOLUME: 167
 (F) PAGES: 554-557
 (G) DATE: 1988
 (K) RELEVANT RESIDUES IN SEQ ID NO:25: FROM 1 TO 1027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGCAAAAGCA GGUAGAUUU GAAAG AUG AGU CUU CUA ACC GAG GUC GAA ACG	52
Met Ser Leu Leu Thr Glu Val Glu Thr	
1 5	
UAC GUU CUC UCU AUC AUC CCG UCA GGC CCC CUC AAA GCC GAG AUC GCA	100
Tyr Val Leu Ser Ile Ile Pro Ser Gly Pro Leu Lys Ala Glu Ile Ala	
10 15 20 25	
CAG AGA CUU GAA GAU GUC UUU GCU GGG AAA AAC ACC GAU CUU GAG GCU	148
Gln Arg Leu Glu Asp Val Phe Ala Gly Lys Asn Thr Asp Leu Glu Ala	
30 35 40	
CUC AUG GAA UGG CUA AAG ACA AGA CCA AUC CUG UCA CCU CUG ACU AAG	196
Leu Met Glu Trp Leu Lys Thr Arg Pro Ile Leu Ser Pro Leu Thr Lys	
45 50 55	
GGG AUU UUG GGA UUU GUA UUC ACG CUC ACC GUG CCC AGU GAG CGA GGA	244
Gly Ile Leu Gly Phe Val Phe Thr Leu Thr Val Pro Ser Glu Arg Gly	
60 65 70	
CUG CAG CGU AGA CGC UUU GUC CAA AAU GCC CUC AAU GGG AAU GGG GAU	292
Leu Gln Arg Arg Arg Phe Val Gln Asn Ala Leu Asn Gly Asn Gly Asp	
75 80 85	
CCA AAU AAC AUG GAC AGA GCA GUU AAA CUG UAU AGA AAG CUU AAG AGG	340
Pro Asn Asn Met Asp Arg Ala Val Lys Leu Tyr Arg Lys Leu Lys Arg	

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90	95	100	105	
GAG AUA ACA UUC CAU GGG GCC AAA GAA AUA GCG CUC AGU UAU UCU GCU				388
Glu Ile Thr Phe His 110	Gly Ala Lys Glu Ile 115	Ala Leu Ser Tyr	Ser Ala 120	
GGU GCA CUU GCC AGU UGU AUG GGC CUC AUA UAC AAC AGG AUG GGG GCU				436
Gly Ala Leu Ala 125	Ser Cys Met Gly Leu 130	Ile Tyr Asn Arg Met 135	Gly Ala	
GUG ACC ACU GAA GUG GUC UUA GGC CUG GUA UGU GCA ACC UGU GAA CAG				484
Val Thr Thr Glu Val Val Leu Gly 145	Leu Val Cys Ala Thr 150	Cys Glu Gln		
AUU GCU GAC UCC CAG CAU AGG UCU CAU AGG CAA AUG GUG ACA ACA ACC				532
Ile Ala Asp Ser Gln His Arg 160	Ser His Arg Gln Met 165	Val Thr Thr		
AAU CCA CUA AUA AGA CAU GAG AAC AGA AUG GUU CUG GCC AGC ACU ACA				580
Asn Pro Leu Ile Arg His 175	Glu Asn Arg Met Val 180	Leu Ala Ser Thr Thr 185		
GCU AAG GCU AUG GAG CAA AUG GCU GGA UCG AGU GAG CAA GCA GCA GAG				628
Ala Lys Ala Met Glu Gln Met Ala Gly Ser 195	Ser Glu Gln Ala GCA GAG			
GCC AUG GAG GUU GCU AGU CAG GCC AGG CAA AUG GUG CAG GCA AUG AGA				676
Ala Met Glu Val Ala Ser Gln Ala Arg 210	Gln Met Val Gln Ala Met Arg			
GUU AUU GGG ACU CAU CCU AGC UCC AGU GCU GGU CUA AAA AAU GAU CUU				724
Val Ile Gly Thr His Pro Ser Ser 225	Ser Ala Gly Leu Lys 230	Asn Asp Leu		
CUU GAA AAU UUG CAG GCC UAU CAG AAA CGA AUG GGG GUG CAG AUG CAA				772
Leu Glu Asn Leu Gln Ala Tyr Gln Lys Arg Met Gly Val Gln Met Gln				
CGA UUC AAG UGACCCUCUU GUUGUUGCCG CGAGUAUCAU UGGGAUCUUG				821
Arg Phe Lys 250				
CACUUGAUU UGUGGAUUCU UGAUCAUCUU UUUUUCAAAU GCAUUUAUCG CUUCUUUAAA				881
CACGGUCUGA AAAGAGGGCC UUCUACGGAA GGAGUACCAG AGUCUAUGAG GGAAGAAUUA				941
CGAAAGGAAC AGCAGAGUGC UGUGGAUUCU GACGAUAGUC AUUUUGUCAG CAUAGAGCUG				1001
GAGUAAAAAA CUACCUUGUU UCUACU				1027

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ser Leu Leu Thr Glu Val Glu Thr Tyr Val Leu Ser Ile Ile Pro

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```

1           5           10           15
Ser Gly Pro Leu Lys Ala Glu Ile Ala Gln Arg Leu Glu Asp Val Phe
          20          25          30
Ala Gly Lys Asn Thr Asp Leu Glu Ala Leu Met Glu Trp Leu Lys Thr
          35          40          45
Arg Pro Ile Leu Ser Pro Leu Thr Lys Gly Ile Leu Gly Phe Val Phe
          50          55          60
Thr Leu Thr Val Pro Ser Glu Arg Gly Leu Gln Arg Arg Arg Phe Val
          65          70          75          80
Gln Asn Ala Leu Asn Gly Asn Gly Asp Pro Asn Asn Met Asp Arg Ala
          85          90          95
Val Lys Leu Tyr Arg Lys Leu Lys Arg Glu Ile Thr Phe His Gly Ala
          100         105         110
Lys Glu Ile Ala Leu Ser Tyr Ser Ala Gly Ala Leu Ala Ser Cys Met
          115         120         125
Gly Leu Ile Tyr Asn Arg Met Gly Ala Val Thr Thr Glu Val Val Leu
          130         135         140
Gly Leu Val Cys Ala Thr Cys Glu Gln Ile Ala Asp Ser Gln His Arg
          145         150         155         160
Ser His Arg Gln Met Val Thr Thr Thr Asn Pro Leu Ile Arg His Glu
          165         170         175
Asn Arg Met Val Leu Ala Ser Thr Thr Ala Lys Ala Met Glu Gln Met
          180         185         190
Ala Gly Ser Ser Glu Gln Ala Ala Glu Ala Met Glu Val Ala Ser Gln
          195         200         205
Ala Arg Gln Met Val Gln Ala Met Arg Val Ile Gly Thr His Pro Ser
          210         215         220
Ser Ser Ala Gly Leu Lys Asn Asp Leu Leu Glu Asn Leu Gln Ala Tyr
          225         230         235         240
Gln Lys Arg Met Gly Val Gln Met Gln Arg Phe Lys
          245         250

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 26..316
- (D) OTHER INFORMATION: /product= "Matrix M2"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGCAAAAGCA	GGUAGAUUU	GAAAG	AUG	AGU	CUU	CUA	ACC	GAG	GUC	GAA	ACG		52			
			Met	Ser	Leu	Leu	Thr	Glu	Val	Glu	Thr					
			1				5									
CCU	AUC	AGA	AAC	GAA	UGG	GGG	UGC	AGA	UGC	AAC	GAU	UCA	AGU	GAC	CCU	100
Pro	Ile	Arg	Asn	Glu	Trp	Gly	Cys	Arg	Cys	Asn	Asp	Ser	Ser	Asp	Pro	
10					15					20					25	
CUU	GUU	GUU	GCC	GCG	AGU	AUC	AUU	GGG	AUC	UUG	CAC	UUG	AUA	UUG	UGG	148
Leu	Val	Val	Ala	Ala	Ser	Ile	Ile	Gly	Ile	Leu	His	Leu	Ile	Leu	Trp	
			30					35					40			
AUU	CUU	GAU	CAU	CUU	UUU	UUC	AAA	UGC	AUU	UAU	CGC	UUC	UUU	AAA	CAC	196
Ile	Leu	Asp	His	Leu	Phe	Phe	Lys	Cys	Ile	Tyr	Arg	Phe	Phe	Lys	His	
			45					50					55			
GGU	CUG	AAA	AGA	GGG	CCU	UCU	ACG	GAA	GGA	GUA	CCA	GAG	UCU	AUG	AGG	244
Gly	Leu	Lys	Arg	Gly	Pro	Ser	Thr	Glu	Gly	Val	Pro	Glu	Ser	Met	Arg	
		60					65					70				
GAA	GAA	UAU	CGA	AAG	GAA	CAG	CAG	AGU	GCU	GUG	GAU	UCU	GAC	GAU	AGU	292
Glu	Glu	Tyr	Arg	Lys	Glu	Gln	Gln	Ser	Ala	Val	Asp	Ser	Asp	Asp	Ser	
	75					80					85					
CAU	UUU	GUC	AGC	AUA	GAG	CUG	GAG	UAAAAACUA	CCUUGUUUCU	ACU						339
His	Phe	Val	Ser	Ile	Glu	Leu	Glu									
90					95											

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Ser	Leu	Leu	Thr	Glu	Val	Glu	Thr	Pro	Ile	Arg	Asn	Glu	Trp	Gly	
1				5					10					15		
Cys	Arg	Cys	Asn	Asp	Ser	Ser	Asp	Pro	Leu	Val	Val	Ala	Ala	Ser	Ile	
			20					25					30			
Ile	Gly	Ile	Leu	His	Leu	Ile	Leu	Trp	Ile	Leu	Asp	His	Leu	Phe	Phe	
		35					40					45				
Lys	Cys	Ile	Tyr	Arg	Phe	Phe	Lys	His	Gly	Leu	Lys	Arg	Gly	Pro	Ser	
	50					55					60					
Thr	Glu	Gly	Val	Pro	Glu	Ser	Met	Arg	Glu	Glu	Tyr	Arg	Lys	Glu	Gln	
	65				70					75					80	
Gln	Ser	Ala	Val	Asp	Ser	Asp	Asp	Ser	His	Phe	Val	Ser	Ile	Glu	Leu	
			85						90					95		
Glu																

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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) egg passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PB2

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(141, "a")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain; a in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(426, "c")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain and in wt2(3); u in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(714, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3); c in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(821, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(963, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1182, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1212, "u")

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- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3);
c in 1988 reported wild type E28-32 strain"
/citation= ([1][2])
- (ix) FEATURE:
(A) NAME/KEY: conflict
(B) LOCATION: replace(1353, "g")
(D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3);
u in 1988 reported wild type E28-32 strain"
/citation= ([1][2])
- (ix) FEATURE:
(A) NAME/KEY: conflict
(B) LOCATION: replace(1923, "g")
(D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3);
a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])
- (ix) FEATURE:
(A) NAME/KEY: mutation
(B) LOCATION: replace(1933, "u")
(D) OTHER INFORMATION: /note= "c in ca "master" strain; u in wt2(3); u
in 1988 reported wild type E28-32 strain"
/citation= ([1][2])
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 28..2304
(D) OTHER INFORMATION: /product= "polymerase basic 2"
/gene= "PB2"
/note= "polymerase basic 2"
/citation= ([1][2])
- (x) PUBLICATION INFORMATION:
(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
(B) TITLE: Molecular and biological changes in the cold
adapted master strain A/AA/6/60 (H2N2) influenza
virus
(C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
(G) DATE: 1993
(K) RELEVANT RESIDUES IN SEQ ID NO:29: FROM 1 TO 2341
- (x) PUBLICATION INFORMATION:
(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C
(B) TITLE: Identification of sequence changes in the
cold-adapted live attenuated influenza vaccine
strain, A/Ann Arbor/6/60(H2N2)
(C) JOURNAL: Virology
(D) VOLUME: 167
(F) PAGES: 554-567
(G) DATE: 1988
(K) RELEVANT RESIDUES IN SEQ ID NO:29: FROM 1 TO 2341
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

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Met Glu Arg Ile Lys Glu Leu Arg

1

5

AAU CUG AUG UCG CAG UCU CGC ACU CGC GAG AUA CUA ACA AAA ACC ACA Asn Leu Met Ser Gln Ser Arg Thr Arg Glu Ile Leu Thr Lys Thr Thr	99
10 15 20	
GUG GAC CAU AUG GCC AUA AUU AAG AAG UAC ACA UCA GGG AGA CAG GAA Val Asp His Met Ala Ile Ile Lys Lys Tyr Thr Ser Gly Arg Gln Glu	147
25 30 35 40	
AAG AAC CCG UCA CUU AGG AUG AAA UGG AUG AUG GCA AUG AAA UAU CCG Lys Asn Pro Ser Leu Arg Met Lys Trp Met Met Ala Met Lys Tyr Pro	195
45 50 55	
AUU ACA GCC GAC AAG AGG AUA ACA GAA AUG AUU CCU GAG AGA AAU GAG Ile Thr Ala Asp Lys Arg Ile Thr Glu Met Ile Pro Glu Arg Asn Glu	243
60 65 70	
CAA GGG CAA ACU CUA UGG AGU AAA AUG AGU GAU GCC GGA UCG GAU CGU Gln Gly Gln Thr Leu Trp Ser Lys Met Ser Asp Ala Gly Ser Asp Arg	291
75 80 85	
GUG AUG GUA UCA CCU CUG GCU GUG ACA UGG UGG AAU AGA AAU GGA CCA Val Met Val Ser Pro Leu Ala Val Thr Trp Trp Asn Arg Asn Gly Pro	339
90 95 100	
AUG ACA AGU ACG GUU CAU UAU CCA AAA AUC UAC AAA ACU UAU UUU GAG Met Thr Ser Thr Val His Tyr Pro Lys Ile Tyr Lys Thr Tyr Phe Glu	387
105 110 115 120	
AAA GUC GAA AGG UUA AAA CAU GGA ACC UUU GGC CCU GUC CAU UUU AGA Lys Val Glu Arg Leu Lys His Gly Thr Phe Gly Pro Val His Phe Arg	435
125 130 135	
AAC CAA GUC AAA AUA CGC CGA AGA GUU GAC AUA AAU CCU GGU CAU GCA Asn Gln Val Lys Ile Arg Arg Arg Val Asp Ile Asn Pro Gly His Ala	483
140 145 150	
GAC CUC AGU GCC AAG GAG GCA CAG GAU GUA AUC AUG GAA GUU GUU UUC Asp Leu Ser Ala Lys Glu Ala Gln Asp Val Ile Met Glu Val Val Phe	531
155 160 165	
CCU AAC GAA GUG GGG GCC AGG AUA CUA ACG UCG GAA UCG CAA UUA ACA Pro Asn Glu Val Gly Ala Arg Ile Leu Thr Ser Glu Ser Gln Leu Thr	579
170 175 180	
AUA ACC AAA GAG AAA AAA GAA GAA CUC CAG GAU UGC AAA AUU UCA CCU Ile Thr Lys Glu Lys Lys Glu Glu Leu Gln Asp Cys Lys Ile Ser Pro	627
185 190 195 200	
UUG AUG GUU GCG UAC AUG UUA GAG AGA GAA CUU GUC CGA AAA ACG AGA Leu Met Val Ala Tyr Met Leu Glu Arg Glu Leu Val Arg Lys Thr Arg	675
205 210 215	
UUU CUC CCA GUU GCU GGU GGA ACA AGC AGU GUG UAC AUU GAA GUG UUG Phe Leu Pro Val Ala Gly Gly Thr Ser Ser Val Tyr Ile Glu Val Leu	723
220 225 230	
CAC UUG ACU CAA GGA ACA UGC UGG GAA CAG AUG UAC ACU CCA GGU GGA His Leu Thr Gln Gly Thr Cys Trp Glu Gln Met Tyr Thr Pro Gly Gly	771
235 240 245	
GAA GUG AGG AAU GAU GAU GUU GAU CAA AGU CUA AUU AUU GCA GCC AGG	819

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Glu Val Arg Asn Asp Asp Val Asp Gln Ser Leu Ile Ile Ala Ala Arg	
250 255 260	
AGC AUA GUG AGA AGA GCA GCA GUA UCA GCA GAU CCA CUA GCA UCU UUA	867
Ser Ile Val Arg Arg Ala Ala Val Ser Ala Asp Pro Leu Ala Ser Leu	
265 270 275 280	
UUG GAG AUG UGC CAC AGC ACA CAG AUU GGC GGG ACA AGG AUG GUG GAC	915
Leu Glu Met Cys His Ser Thr Gln Ile Gly Gly Thr Arg Met Val Asp	
285 290 295	
AUU CUU AGG CAG AAC CCA ACA GAA GAG CAA GCU GUG GAA AUA UGC AAG	963
Ile Leu Arg Gln Asn Pro Thr Glu Glu Gln Ala Val Glu Ile Cys Lys	
300 305 310	
GCU GCA AUG GGA CUG AGG AUC AGC UCA UCC UUC AGU UUU GGC GGG UUC	1011
Ala Ala Met Gly Leu Arg Ile Ser Ser Ser Phe Ser Phe Gly Gly Phe	
315 320 325	
ACA UUU AAG AGA ACA AGC GGA UCA UCA GUC AAG AGA GAG GAA GAA GUG	1059
Thr Phe Lys Arg Thr Ser Gly Ser Ser Val Lys Arg Glu Glu Glu Val	
330 335 340	
CUU ACG GGC AAU CUU CAA ACA UUG AAA AUA AGG GUG CAU GAG GGA UAC	1107
Leu Thr Gly Asn Leu Gln Thr Leu Lys Ile Arg Val His Glu Gly Tyr	
345 350 355 360	
GAG GAG UUC ACA AUG GUU GGG AAA AGG GCA ACA GCU AUA CUC AGA AAA	1155
Glu Glu Phe Thr Met Val Gly Lys Arg Ala Thr Ala Ile Leu Arg Lys	
365 370 375	
GCA ACC AGG AGA UUG AUU CAG CUG AUU GUG AGU GGA AGA GAC GAA CAG	1203
Ala Thr Arg Arg Leu Ile Gln Leu Ile Val Ser Gly Arg Asp Glu Gln	
380 385 390	
UCG AUA GCU GAA GCA AUA AUU GUG GCC AUG GUA UUU UCA CAA GAA GAU	1251
Ser Ile Ala Glu Ala Ile Ile Val Ala Met Val Phe Ser Gln Glu Asp	
395 400 405	
UGU AUG AUA AAA GCA GUU AGA GGU GAU CUG AAU UUC GUU AAU AGG GCA	1299
Cys Met Ile Lys Ala Val Arg Gly Asp Leu Asn Phe Val Asn Arg Ala	
410 415 420	
AAU CAG CGA UUG AAU CCC AUG CAU CAA CUU UUA AGA CAU UUU CAG AAG	1347
Asn Gln Arg Leu Asn Pro Met His Gln Leu Leu Arg His Phe Gln Lys	
425 430 435 440	
GAU GCG AAA GUG CUU UUU CAA AAU UGG GGA AUU GAA CAU AUC GAC AAU	1395
Asp Ala Lys Val Leu Phe Gln Asn Trp Gly Ile Glu His Ile Asp Asn	
445 450 455	
GUG AUG GGA AUG AUU GGG GUA UUA CCA GAC AUG ACU CCA AGC ACA GAG	1443
Val Met Gly Met Ile Gly Val Leu Pro Asp Met Thr Pro Ser Thr Glu	
460 465 470	
AUG UCA AUG AGA GGG GUA AGA GUC AGC AAA AUG GGC GUA GAU GAA UAC	1491
Met Ser Met Arg Gly Val Arg Val Ser Lys Met Gly Val Asp Glu Tyr	
475 480 485	
UCC AGC GCG GAG AGA GUA GUG GUG AGC AUU GAC CGG UUU UUG AGA GUU	1539
Ser Ser Ala Glu Arg Val Val Val Ser Ile Asp Phe Leu Arg Val	
490 495 500	

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CGA Arg 505	GAC Asp	CAA Gln	CGA Arg	GGA Gly	AAU Asn 510	GUA Val	CUA Leu	CUA Leu	UCU Ser	CCU Pro 515	GAG Glu	GAG Glu	GUC Val	AGU Ser	GAA Glu 520	1587
ACA Thr	CAG Gln	GGA Gly	ACA Thr	GAG Glu 525	AAA Lys	CUG Leu	ACA Thr	AUA Ile	ACU Thr 530	UAC Tyr	UCA Ser	UCG Ser	UCA Ser	AUG Met 535	AUG Met	1635
UGG Trp	GAG Glu	AUU Ile	AAU Asn 540	GGC Gly	CCU Pro	GAG Glu	UCA Ser	GUG Val 545	UUG Leu	GUC Val	AAU Asn	ACC Thr	UAU Tyr 550	CAG Gln	UGG Trp	1683
AUC Ile	AUC Ile	AGA Arg 555	AAC Asn	UGG Trp	GAA Glu	ACU Thr	GUU Val 560	AAA Lys	AUU Ile	CAG Gln	UGG Trp	UCU Ser 565	CAG Gln	AAU Asn	CCU Pro	1731
ACA Thr 570	AUG Met	CUA Leu	UAC Tyr	AAU Asn	AAA Lys	AUG Met 575	GAA Glu	UUU Phe	GAG Glu	CCA Pro	UUU Phe 580	CAG Gln	UCU Ser	UUA Leu	GUU Val	1779
CCU Pro 585	AAG Lys	GCC Ala	AUU Ile	AGA Arg	GGC Gly 590	CAA Gln	UAC Tyr	AGU Ser	GGG Gly 595	UUU Phe	GUU Val	AGG Arg	ACU Thr	CUA Leu	UUC Phe 600	1827
CAA Gln	CAA Gln	AUG Met	AGG Arg	GAU Asp 605	GUA Val	CUU Leu	GGG Gly	ACA Thr	UUU Phe 610	GAU Asp	ACC Thr	ACC Thr	CAG Gln	AUA Ile 615	AUA Ile	1875
AAA Lys	CUU Leu	CUU Leu	CCC Pro 620	UUU Phe	GCA Ala	GCC Ala	GCC Ala	CCA Pro 625	CCA Pro	AAG Lys	CAA Gln	AGU Ser	AGA Arg 630	AUG Met	CAG Gln	1923
UUC Phe	UCU Ser	UCA Ser 635	UUG Leu	ACU Thr	GUG Val	AAU Asn	GUG Val 640	AGG Arg	GGA Gly	UCA Ser	GGA Gly	AUG Met 645	AGA Arg	AUA Ile	CUU Leu	1971
GUA Val 650	AGG Arg	GGC Gly	AAU Asn	UCU Ser	CCU Pro	AUA Ile 655	UUC Phe	AAC Asn	UAC Tyr	AAC Asn	AAG Lys 660	ACC Thr	ACU Thr	AAG Lys	AGA Arg	2019
CUA Leu 665	ACA Thr	AUU Ile	CUC Leu	GGA Gly	AAG Lys 670	GAU Asp	GCU Ala	GGC Gly	ACU Thr	UUA Leu 675	ACU Thr	GAA Glu	GAC Asp	CCA Pro	GAU Asp 680	2067
GAA Glu	GGC Gly	ACA Thr	UCU Ser	GGA Gly 685	GUG Val	GAG Glu	UCC Ser	GCU Ala	GUU Val 690	CUG Leu	AGA Arg	GGA Gly	UUC Phe	CUC Leu 695	AUU Ile	2115
CUG Leu	GGC Gly	AAA Lys	GAA Glu 700	GAU Asp	AGG Arg	AGA Arg	UAU Tyr	GGA Gly 705	CCA Pro	GCA Ala	UUA Leu	AGC Ser	AUC Ile 710	AAU Asn	GAA Glu	2163
CUG Leu	AGU Ser	AAC Asn 715	CUU Leu	GCG Ala	AAA Lys	GGA Gly	GAA Glu 720	AAG Lys	GCU Ala	AAU Asn	GUA Val 725	CUA Leu 725	AUU Ile	GGG Gly	CAA Gln	2211
GGA Gly 730	GAC Asp	GUG Val	GUG Val	UUG Leu	GUA Val	AUG Met 735	AAA Lys	CGA Arg	AAA Lys	CGG Arg	AAC Asn 740	UCU Ser	AGC Ser	AUA Ile	CUU Leu	2259
ACU Thr 745	GAC Asp	AGC Ser	CAG Gln	ACA Thr	GCG Ala 750	ACC Thr	AAA Lys	AGG Arg	AUU Ile	CGG Arg 755	AUG Met	GCC Ala	AUC Ile	AAU Asn		2304

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UAAUGUUGAA UAGUUUAAAA ACGACCUUGU UUCUACU

2341

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

Met Glu Arg Ile Lys Glu Leu Arg Asn Leu Met Ser Gln Ser Arg Thr
 1           5           10
Arg Glu Ile Leu Thr Lys Thr Thr Val Asp His Met Ala Ile Ile Lys
          20           25           30
Lys Tyr Thr Ser Gly Arg Gln Glu Lys Asn Pro Ser Leu Arg Met Lys
          35           40           45
Trp Met Met Ala Met Lys Tyr Pro Ile Thr Ala Asp Lys Arg Ile Thr
          50           55           60
Glu Met Ile Pro Glu Arg Asn Glu Gln Gly Gln Thr Leu Trp Ser Lys
          65           70           75           80
Met Ser Asp Ala Gly Ser Asp Arg Val Met Val Ser Pro Leu Ala Val
          85           90           95
Thr Trp Trp Asn Arg Asn Gly Pro Met Thr Ser Thr Val His Tyr Pro
          100          105          110
Lys Ile Tyr Lys Thr Tyr Phe Glu Lys Val Glu Arg Leu Lys His Gly
          115          120          125
Thr Phe Gly Pro Val His Phe Arg Asn Gln Val Lys Ile Arg Arg Arg
          130          135          140
Val Asp Ile Asn Pro Gly His Ala Asp Leu Ser Ala Lys Glu Ala Gln
          145          150          155          160
Asp Val Ile Met Glu Val Val Phe Pro Asn Glu Val Gly Ala Arg Ile
          165          170          175
Leu Thr Ser Glu Ser Gln Leu Thr Ile Thr Lys Glu Lys Lys Glu Glu
          180          185          190
Leu Gln Asp Cys Lys Ile Ser Pro Leu Met Val Ala Tyr Met Leu Glu
          195          200          205
Arg Glu Leu Val Arg Lys Thr Arg Phe Leu Pro Val Ala Gly Gly Thr
          210          215          220
Ser Ser Val Tyr Ile Glu Val Leu His Leu Thr Gln Gly Thr Cys Trp
          225          230          235          240
Glu Gln Met Tyr Thr Pro Gly Gly Glu Val Arg Asn Asp Asp Val Asp
          245          250          255

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Gln Ser Leu Ile Ile Ala Ala Arg Ser Ile Val Arg Arg Ala Ala Val
260 265 270

Ser Ala Asp Pro Leu Ala Ser Leu Leu Glu Met Cys His Ser Thr Gln
275 280 285

Ile Gly Gly Thr Arg Met Val Asp Ile Leu Arg Gln Asn Pro Thr Glu
290 295 300

Glu Gln Ala Val Glu Ile Cys Lys Ala Ala Met Gly Leu Arg Ile Ser
305 310 315 320

Ser Ser Phe Ser Phe Gly Gly Phe Thr Phe Lys Arg Thr Ser Gly Ser
325 330 335

Ser Val Lys Arg Glu Glu Glu Val Leu Thr Gly Asn Leu Gln Thr Leu
340 345 350

Lys Ile Arg Val His Glu Gly Tyr Glu Glu Phe Thr Met Val Gly Lys
355 360 365

Arg Ala Thr Ala Ile Leu Arg Lys Ala Thr Arg Arg Leu Ile Gln Leu
370 375 380

Ile Val Ser Gly Arg Asp Glu Gln Ser Ile Ala Glu Ala Ile Ile Val
385 390 395 400

Ala Met Val Phe Ser Gln Glu Asp Cys Met Ile Lys Ala Val Arg Gly
405 410 415

Asp Leu Asn Phe Val Asn Arg Ala Asn Gln Arg Leu Asn Pro Met His
420 425 430

Gln Leu Leu Arg His Phe Gln Lys Asp Ala Lys Val Leu Phe Gln Asn
435 440 445

Trp Gly Ile Glu His Ile Asp Asn Val Met Gly Met Ile Gly Val Leu
450 455 460

Pro Asp Met Thr Pro Ser Thr Glu Met Ser Met Arg Gly Val Arg Val
465 470 475 480

Ser Lys Met Gly Val Asp Glu Tyr Ser Ser Ala Glu Arg Val Val Val
485 490 495

Ser Ile Asp Arg Phe Leu Arg Val Arg Asp Gln Arg Gly Asn Val Leu
500 505 510

Leu Ser Pro Glu Glu Val Ser Glu Thr Gln Gly Thr Glu Lys Leu Thr
515 520 525

Ile Thr Tyr Ser Ser Ser Met Met Trp Glu Ile Asn Gly Pro Glu Ser
530 535 540

Val Leu Val Asn Thr Tyr Gln Trp Ile Ile Arg Asn Trp Glu Thr Val
545 550 555 560

Lys Ile Gln Trp Ser Gln Asn Pro Thr Met Leu Tyr Asn Lys Met Glu
565 570 575

Phe Glu Pro Phe Gln Ser Leu Val Pro Lys Ala Ile Arg Gly Gln Tyr
580 585 590

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Ser Gly Phe Val Arg Thr Leu Phe Gln Gln Met Arg Asp Val Leu Gly
595 600 605

Thr Phe Asp Thr Thr Gln Ile Ile Lys Leu Leu Pro Phe Ala Ala Ala
610 615 620

Pro Pro Lys Gln Ser Arg Met Gln Phe Ser Ser Leu Thr Val Asn Val
625 630 635 640

Arg Gly Ser Gly Met Arg Ile Leu Val Arg Gly Asn Ser Pro Ile Phe
645 650 655

Asn Tyr Asn Lys Thr Thr Lys Arg Leu Thr Ile Leu Gly Lys Asp Ala
660 665 670

Gly Thr Leu Thr Glu Asp Pro Asp Glu Gly Thr Ser Gly Val Glu Ser
675 680 685

Ala Val Leu Arg Gly Phe Leu Ile Leu Gly Lys Glu Asp Arg Arg Tyr
690 695 700

Gly Pro Ala Leu Ser Ile Asn Glu Leu Ser Asn Leu Ala Lys Gly Glu
705 710 715 720

Lys Ala Asn Val Leu Ile Gly Gln Gly Asp Val Val Leu Val Met Lys
725 730 735

Arg Lys Arg Asn Ser Ser Ile Leu Thr Asp Ser Gln Thr Ala Thr Lys
740 745 750

Arg Ile Arg Met Ala Ile Asn
755

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PB1

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(123, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3);
a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(486, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3);
c in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

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- (ix) FEATURE:
 (A) NAME/KEY: conflict
 (B) LOCATION: replace(1195, "g")
 (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3);
 a in 1988 reported wild type E28-32 strain"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: mutation
 (B) LOCATION: replace(1276, "a")
 (D) OTHER INFORMATION: /note= "g in ca "master" strain; a in wt2(3); g
 in 1988 reported wild type E28-32 strain"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: conflict
 (B) LOCATION: replace(1395, "u")
 (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3);
 g in 1988 reported wild type E28-32 strain"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: conflict
 (B) LOCATION: replace(1766, "g")
 (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3);
 a in 1988 reported wild type E28-32 strain"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: conflict
 (B) LOCATION: replace(2005, "a")
 (D) OTHER INFORMATION: /note= "a in ca "master" strain and in wt2(3);
 g in 1988 reported wild type E28-32 strain"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: conflict
 (B) LOCATION: replace(2019, "u")
 (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3);
 c in 1988 reported wild type E28-32 strain"
 /citation= ([1][2])
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 25..2295
 (D) OTHER INFORMATION: /product= "polymerase basic 1"
 /gene= "PB1"
 /note= "polymerase basic 1"
 /citation= ([1][2])
- (x) PUBLICATION INFORMATION:
 (A) AUTHORS: Herlocher, M L
 Maassab, H F
 Webster, R G
 (B) TITLE: Molecular and biological changes in the cold
 adapted master strain A/AA/6/60 (H2N2) influenza
 virus
 (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
 (G) DATE: 1993
 (K) RELEVANT RESIDUES IN SEQ ID NO:31: FROM 1 TO 2341
- (x) PUBLICATION INFORMATION:

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(A) AUTHORS: Cox, N J
 Kitame, F
 Kendal, A P
 Maassab, H F
 Naeve, C
 (B) TITLE: Identification of sequence changes in the
 cold-adapted live attenuated influenza vaccine
 strain
 (C) JOURNAL: Virology
 (D) VOLUME: 167
 (F) PAGES: 554-567
 (G) DATE: 1988
 (K) RELEVANT RESIDUES IN SEQ ID NO:31: FROM 1 TO 2341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGCGAAAGCA GGCAAACCAU UUGA AUG GAU GUC AAU CCG ACC UUA CUU UUC	51
Met Asp Val Asn Pro Thr Leu Leu Phe	
1 5	
UUG AAA GUU CCA GCG CAA AAU GCC AUA AGU ACU ACA UUC CCU UAU ACU	99
Leu Lys Val Pro Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr	
10 15 20 25	
GGA GAU CCU CCA UAC AGC CAU GGG ACA GGA ACA GGA UAC ACC AUG GAC	147
Gly Asp Pro Pro Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp	
30 35 40	
ACA GUC AAC AGA ACA CAU CAA UAU UCA GAA AAG GGG AAG UGG ACA ACA	195
Thr Val Asn Arg Thr His Gln Tyr Ser Glu Lys Gly Lys Trp Thr Thr	
45 50 55	
AAC ACG GAA ACU GGA GCG CAC CAA CUU AAC CCA AUU GAU GGA CCA CUA	243
Asn Thr Glu Thr Gly Ala His Gln Leu Asn Pro Ile Asp Gly Pro Leu	
60 65 70	
CCU GAG GAC AAU GAA CCA AGU GGA UAU GCA CAA ACA GAC UGC GUC CUG	291
Pro Glu Asp Asn Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu	
75 80 85	
GAA GCA AUG GCU UUC CUU GAA GAA UCC CAC CCA GGA AUC UUU GAA AAC	339
Glu Ala Met Ala Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Asn	
90 95 100 105	
UCG UGU CUU GAA ACG AUG GAA GUU AUU CAA CAA ACA AGA GUG GAC AAA	387
Ser Cys Leu Glu Thr Met Glu Val Ile Gln Gln Thr Arg Val Asp Lys	
110 115 120	
CUG ACC CAA GGU CGU CAG ACC UAU GAU UGG ACA UUG AAC AGA AAU CAG	435
Leu Thr Gln Gly Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln	
125 130 135	
CCG GCU GCA ACU GCG CUA GCC AAC ACU AUA GAG GUC UUC AGA UCG AAU	483
Pro Ala Ala Thr Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn	
140 145 150	
GGU CUG ACA GCU AAU GAA UCG GGA AGG CUA AUA GAU UUC CUC AAG GAU	531
Gly Leu Thr Ala Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp	
155 160 165	
GUG AUA GAA UCA AUG GAU AAA GAG GAG AUG GAA AUC ACA ACA CAC UUC	579
Val Ile Glu Ser Met Asp Lys Glu Glu Met Glu Ile Thr Thr His Phe	

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170		175		180		185										
CAA	AGA	AAA	AGA	AGA	GUA	AGA	GAC	AAC	AUG	ACC	AAG	AAA	AUG	GUC	ACA	627
Gln	Arg	Lys	Arg	Arg	Val	Arg	Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	
				190					195					200		
CAA	CGA	ACA	AUA	GGA	AAG	AAG	AAG	CAA	AGA	UUG	AAC	AAG	AGA	AGC	UAU	675
Gln	Arg	Thr	Ile	Gly	Lys	Lys	Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	
			205					210					215			
CUA	AUA	AGA	GCA	CUG	ACA	UUG	AAC	ACA	AUG	ACU	AAA	GAU	GCA	GAG	AGA	723
Leu	Ile	Arg	Ala	Leu	Thr	Leu	Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	
		220					225					230				
GGU	AAA	UUA	AAG	AGA	AGA	GCA	AUU	GCA	ACA	CCC	GGU	AUG	CAG	AUC	AGA	771
Gly	Lys	Leu	Lys	Arg	Arg	Ala	Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	
	235					240					245					
GGG	UUC	GUG	UAC	UUU	GUC	GAA	ACA	CUA	GCG	AGA	AGU	AUU	UGU	GAG	AAG	819
Gly	Phe	Val	Tyr	Phe	Val	Glu	Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	
	250				255					260					265	
CUU	GAA	CAG	UCU	GGG	CUU	CCG	GUU	GGA	GGU	AAU	GAA	AAG	AAG	GCU	AAA	867
Leu	Glu	Gln	Ser	Gly	Leu	Pro	Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	
				270					275					280		
CUG	GCA	AAU	GUU	GUG	CGA	AAA	AUG	AUG	ACU	AAU	UCA	CAA	GAC	ACA	GAG	915
Leu	Ala	Asn	Val	Val	Arg	Lys	Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	
			285					290					295			
CUC	UCU	UUC	ACA	AUU	ACU	GGA	GAC	AAU	ACC	AAA	UGG	AAU	GAG	AAU	CAA	963
Leu	Ser	Phe	Thr	Ile	Thr	Gly	Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	
		300					305					310				
AAU	CCU	CGG	AUG	UUC	CUG	GCG	AUG	AUA	ACA	UAC	AUC	ACA	AGA	AAU	CAA	1011
Asn	Pro	Arg	Met	Phe	Leu	Ala	Met	Ile	Thr	Tyr	Ile	Thr	Arg	Asn	Gln	
	315					320					325					
CCU	GAA	UGG	UUU	AGA	AAC	GUC	CUG	AGC	AUC	GCA	CCU	AUA	AUG	UUC	UCA	1059
Pro	Glu	Trp	Phe	Arg	Asn	Val	Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	
	330				335					340					345	
AAU	AAA	AUG	GCA	AGA	CUA	GGG	AAA	GGA	UAC	AUG	UUC	AAA	AGC	AAG	AGC	1107
Asn	Lys	Met	Ala	Arg	Leu	Gly	Lys	Gly	Tyr	Met	Phe	Lys	Ser	Lys	Ser	
				350					355					360		
AUG	AAG	CUC	CGA	ACA	CAA	AUA	CCA	GCA	GAA	AUG	CUA	GCA	AGU	AUU	GAC	1155
Met	Lys	Leu	Arg	Thr	Gln	Ile	Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	
			365					370					375			
CUG	AAA	UAC	UUU	AAU	GAA	UCA	ACA	AGA	AAG	AAA	AUC	GAG	GAA	AUA	AGG	1203
Leu	Lys	Tyr	Phe	Asn	Glu	Ser	Thr	Arg	Lys	Lys	Ile	Glu	Glu	Ile	Arg	
		380					385					390				
CCU	CUC	CUA	AUA	GAU	GGC	ACA	GUC	UCA	UUG	AGU	CCU	GGA	AUG	AUG	AUG	1251
Pro	Leu	Leu	Ile	Asp	Gly	Thr	Val	Ser	Leu	Ser	Pro	Gly	Met	Met	Met	
		395				400					405					
GGC	AUG	UUC	AAC	AUG	CUA	AGU	ACA	AUC	UUA	GGA	GUC	UCA	AUC	CUG	AAU	1299
Gly	Met	Phe	Asn	Met	Leu	Ser	Thr	Ile	Leu	Gly	Val	Ser	Ile	Leu	Asn	
	410				415					420					425	
CUU	GGA	CAA	AAG	AAG	UAC	ACC	AAA	ACA	ACA	UAC	UGG	UGG	GAC	GGA	CUC	1347

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Leu	Gly	Gln	Lys	Lys	Tyr	Thr	Lys	Thr	Thr	Tyr	Trp	Trp	Asp	Gly	Leu	
				430					435					440		
CAA	UCC	UCU	GAU	GAC	UUC	GCC	CUC	AUA	GUG	AAU	GCA	CCA	AAU	CAU	GAU	1395
Gln	Ser	Ser	Asp	Asp	Phe	Ala	Leu	Ile	Val	Asn	Ala	Pro	Asn	His	Asp	
			445					450					455			
GGA	AUA	CAA	GCA	GGG	GUG	GAU	AGA	UUC	UAC	AGA	ACC	UGC	AAG	CUA	GUC	1443
Gly	Ile	Gln	Ala	Gly	Val	Asp	Arg	Phe	Tyr	Arg	Thr	Cys	Lys	Leu	Val	
		460					465					470				
GGA	AUC	AAU	AUG	AGC	AAA	AAG	AAG	UCC	UAC	AUA	AAU	AGG	ACA	GGG	ACA	1491
Gly	Ile	Asn	Met	Ser	Lys	Lys	Lys	Ser	Tyr	Ile	Asn	Arg	Thr	Gly	Thr	
	475					480					485					
UUU	GAA	UUC	ACA	AGC	UUU	UUC	UAU	CGC	UAU	GGA	UUU	GUA	GCC	AAU	UUU	1539
Phe	Glu	Phe	Thr	Ser	Phe	Phe	Tyr	Arg	Tyr	Gly	Phe	Val	Ala	Asn	Phe	
490					495					500					505	
AGC	AUG	GAG	CUG	CCC	AGC	UUU	GGA	GUG	UCU	GGA	AUU	AAU	GAA	UCG	GCU	1587
Ser	Met	Glu	Leu	Pro	Ser	Phe	Gly	Val	Ser	Gly	Ile	Asn	Glu	Ser	Ala	
				510					515					520		
GAU	AUG	AGC	AUU	GGG	GUA	ACA	GUG	AUA	AAG	AAC	AAC	AUG	AUA	AAC	AAU	1635
Asp	Met	Ser	Ile	Gly	Val	Thr	Val	Ile	Lys	Asn	Asn	Met	Ile	Asn	Asn	
			525					530					535			
GAC	CUU	GGG	CCA	GCA	ACA	GCC	CAA	CUG	GCU	CUU	CAA	CUA	UUC	AUC	AAA	1683
Asp	Leu	Gly	Pro	Ala	Thr	Ala	Gln	Leu	Ala	Leu	Gln	Leu	Phe	Ile	Lys	
		540					545					550				
GAC	UAC	AGA	UAU	ACG	UAC	CGG	UGC	CAC	AGA	GGA	GAC	ACA	CAA	AUU	CAG	1731
Asp	Tyr	Arg	Tyr	Thr	Tyr	Arg	Cys	His	Arg	Gly	Asp	Thr	Gln	Ile	Gln	
	555					560					565					
ACA	AGG	AGA	UCA	UUC	GAG	CUA	AAG	AAG	CUG	UGG	GGG	CAA	ACC	CGC	UCA	1779
Thr	Arg	Arg	Ser	Phe	Glu	Leu	Lys	Lys	Leu	Trp	Gly	Gln	Thr	Arg	Ser	
570					575					580					585	
AAG	GCA	GGA	CUU	UUG	GUU	UCG	GAU	GGA	GGA	CCA	AAC	UUA	UAC	AAU	AUC	1827
Lys	Ala	Gly	Leu	Leu	Val	Ser	Asp	Gly	Gly	Pro	Asn	Leu	Tyr	Asn	Ile	
				590					595					600		
CGG	AAU	CUC	CAC	AUU	CCA	GAA	GUC	UGC	UUG	AAG	UGG	GAG	CUA	AUG	GAU	1875
Arg	Asn	Leu	His	Ile	Pro	Glu	Val	Cys	Leu	Lys	Trp	Glu	Leu	Met	Asp	
			605					610					615			
GAA	GAC	UAU	CAG	GGG	AGG	CUU	UGU	AAU	CCC	CUG	AAU	CCA	UUU	GUC	AGU	1923
Glu	Asp	Tyr	Gln	Gly	Arg	Leu	Cys	Asn	Pro	Leu	Asn	Pro	Phe	Val	Ser	
		620					625					630				
CAU	AAG	GAG	AUU	GAG	UCU	GUA	AAC	AAU	GCU	GUG	GUA	AUG	CCA	GCU	CAC	1971
His	Lys	Glu	Ile	Glu	Ser	Val	Asn	Asn	Ala	Val	Val	Met	Pro	Ala	His	
	635					640					645					
GGU	CCA	GCC	AAG	AGC	AUG	GAA	UAU	GAU	GCU	GUU	ACU	ACU	ACA	CAC	UCU	2019
Gly	Pro	Ala	Lys	Ser	Met	Glu	Tyr	Asp	Ala	Val	Thr	Thr	Thr	His	Ser	
650					655					660					665	
UGG	AUC	CCU	AAG	AGG	AAC	CGC	UCC	AUU	CUC	AAC	ACA	AGC	CAA	AGG	GGA	2067
Trp	Ile	Pro	Lys	Arg	Asn	Arg	Ser	Ile	Leu	Asn	Thr	Ser	Gln	Arg	Gly	
				670					675					680		

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AUU CUU GAA GAU GAA CAG AUG UAU CAG AAG UGU UGC AAU CUA UUC GAG Ile Leu Glu Asp Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu 685 690 695	2115
AAA UUC UUC CCU AGC AGU UCG UAC AGG AGA CCA GUU GGA AUU UCC AGC Lys Phe Phe Pro Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser 700 705 710	2163
AUG GUG GAG GCC AUG GUG UCU AGG GCC CGG AUU GAU GCA CGG AUU GAC Met Val Glu Ala Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp 715 720 725	2211
UUC GAG UCU GGA CGG AUU AAG AAA GAG GAG UUC GCU GAG AUC AUG AAG Phe Glu Ser Gly Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys 730 735 740 745	2259
AUC UGU UCC ACC AUU GAA GAG CUC AGA CGG CAA AAA UAGUGAAUUU Ile Cys Ser Thr Ile Glu Glu Leu Arg Arg Gln Lys 750 755	2305
AGCUUGUCCU UCAUGAAAAA AUGCCUUGUU UCUACU	2341

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 757 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn 1 5 10 15
Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His 20 25 30
Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln 35 40 45
Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr Gly Ala His 50 55 60
Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser 65 70 75 80
Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu 85 90 95
Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu Thr Met Glu 100 105 110
Val Ile Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr 115 120 125
Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala 130 135 140
Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser 145 150 155 160

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Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Ile Glu Ser Met Asp Lys
165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Lys
195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
225 230 235 240

Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
245 250 255

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
260 265 270

Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
275 280 285

Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
290 295 300

Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
305 310 315 320

Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
325 330 335

Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
340 345 350

Lys Gly Tyr Met Phe Lys Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
355 360 365

Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Ser
370 375 380

Thr Arg Lys Lys Ile Glu Glu Ile Arg Pro Leu Leu Ile Asp Gly Thr
385 390 395 400

Val Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
405 410 415

Thr Ile Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Lys Tyr Thr
420 425 430

Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
435 440 445

Leu Ile Val Asn Ala Pro Asn His Asp Gly Ile Gln Ala Gly Val Asp
450 455 460

Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
465 470 475 480

Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
485 490 495

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Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
500 505 510

Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
515 520 525

Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
530 535 540

Gln Leu Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
545 550 555 560

Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
565 570 575

Lys Lys Leu Trp Gly Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
580 585 590

Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
595 600 605

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
610 615 620

Cys Asn Pro Leu Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
625 630 635 640

Asn Asn Ala Val Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
645 650 655

Tyr Asp Ala Val Thr Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
725 730 735

Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
740 745 750

Leu Arg Arg Gln Lys
755

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus

(B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

(B) CLONE: PA

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(20, "c")

(D) OTHER INFORMATION: /note= "c in ca "master" strain and in wt2(3);
u in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(75, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3);
u in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1861, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3);
a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(2167..2168, "cc")

(D) OTHER INFORMATION: /note= "cc in ca "master" strain and in wt2(3);
uu in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 25..2172

(D) OTHER INFORMATION: /product= "polymerase acidic
protein"
/gene= "PA"
/note= "polymerase acidic protein"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L

Maassab, H F

Webster, R G

(B) TITLE: Molecular and biological changes in the cold
adapted master strain A/AA/6/60 (H2N2) influenza
virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:33: FROM 1 TO 2233

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J

Kitame, F

Kendal, A P

Maassab, H F

Naeve, C

(B) TITLE: Identification of sequence changes in the
cold-adapted live attenuated influenza strain,
A/Ann Arbor/6/60(H2N2)

(C) JOURNAL: Virology

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(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:33: FROM 1 TO 2233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGCGAAAGCA GGUACUGAUC CGAA AUG GAA GAU UUU GUG CGA CAA UGC UUC	51
Met Glu Asp Phe Val Arg Gln Cys Phe	
1 5	
AAU CCG AUG AUU GUC GAG CUU GCG GAA AAA GCA AUG AAA GAG UAU GGA	99
Asn Pro Met Ile Val Glu Leu Ala Glu Lys Ala Met Lys Glu Tyr Gly	
10 15 20 25	
GAG GAU CUG AAA AUC GAA ACA AAC AAA UUU GCA GCA AUA UGC ACU CAC	147
Glu Asp Leu Lys Ile Glu Thr Asn Lys Phe Ala Ala Ile Cys Thr His	
30 35 40	
UUG GAA GUA UGC UUC AUG UAU UCA GAU UUU CAU UUC AUC AAU GAG CAA	195
Leu Glu Val Cys Phe Met Tyr Ser Asp Phe His Phe Ile Asn Glu Gln	
45 50 55	
GGC GAG UCA AUA AUA GUA GAG CUU GAU GAU CCA AAU GCA CUU UUG AAG	243
Gly Glu Ser Ile Ile Val Glu Leu Asp Asp Pro Asn Ala Leu Leu Lys	
60 65 70	
CAC AGA UUU GAA AUA AUA GAG GGA AGA GAU CGC ACA AUG GCC UGG ACA	291
His Arg Phe Glu Ile Ile Glu Gly Arg Asp Arg Thr Met Ala Trp Thr	
75 80 85	
GUA GUA AAC AGU AUU UGC AAC ACU ACA GGA GCU GAG AAA CCG AAG UUU	339
Val Val Asn Ser Ile Cys Asn Thr Thr Gly Ala Glu Lys Pro Lys Phe	
90 95 100 105	
CUG CCA GAU UUG UAU GAU UAC AAG GAG AAU AGA UUC AUC GAG AUU GGA	387
Leu Pro Asp Leu Tyr Asp Tyr Lys Glu Asn Arg Phe Ile Glu Ile Gly	
110 115 120	
GUG ACA AGG AGG GAA GUC CAC AUA UAC UAU CUU GAA AAG GCC AAU AAA	435
Val Thr Arg Arg Glu Val His Ile Tyr Tyr Leu Glu Lys Ala Asn Lys	
125 130 135	
AUU AAA UCU GAG AAG ACA CAC AUC CAC AUU UUC UCA UUC ACU GGG GAA	483
Ile Lys Ser Glu Lys Thr His Ile His Ile Phe Ser Phe Thr Gly Glu	
140 145 150	
GAA AUG GCC ACA AAG GCC GAC UAC ACU CUC GAU GAG GAA AGC AGG GCU	531
Glu Met Ala Thr Lys Ala Asp Tyr Thr Leu Asp Glu Glu Ser Arg Ala	
155 160 165	
AGG AUC AAA ACC AGA CUA UUC ACC AUA AGA CAA GAA AUG GCU AGC AGA	579
Arg Ile Lys Thr Arg Leu Phe Thr Ile Arg Gln Glu Met Ala Ser Arg	
170 175 180 185	
GGC CUC UGG GAU UCC UUU CAU CAG UCC GAA AGA GGC GAA GAA ACA AUU	627
Gly Leu Trp Asp Ser Phe His Gln Ser Glu Arg Gly Glu Glu Thr Ile	
190 195 200	
GAA GAA AGA UUU GAA AUC ACA GGG ACA AUG CGC AGG CUC GCC GAC CAA	675
Glu Glu Arg Phe Glu Ile Thr Gly Thr Met Arg Arg Leu Ala Asp Gln	
205 210 215	

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AGU CUC CCG CCG AAC UUC UCC UGC CUU GAG AAU UUU AGA GCC UAU GUG Ser Leu Pro 220 Pro Asn Phe Ser Cys 225 Leu Glu Asn Phe 230 Ala Tyr Val	723
GAU GGA UUC GAA CCG AAC GGC UAC AUU GAG GGC AAG CUU UCU CAA AUG Asp Gly 235 Phe Glu Pro Asn Gly 240 Tyr Ile Glu Gly 245 Lys Leu Ser Gln Met	771
UCC AAA GAA GUA AAU GCU AAA AUU GAA CCU UUU CUG AAA ACA ACA CCA Ser Lys Glu Val Asn Ala 255 Lys Ile Glu Pro Phe 260 Leu Lys Thr Thr Pro 265	819
AGA CCA AUU AGA CUU CCG GAU GGG CCU CCU UGU UCU CAG CGG UCC AAA Arg Pro Ile Arg Leu 270 Pro Asp Gly Pro 275 Cys Ser Gln Arg 280 Ser Lys	867
UUC CUG CUG AUG GAU GCU UUA AAA UUA AGC AUU GAG GAC CCA AGU CAC Phe Leu Leu Met 285 Asp Ala Leu Lys Leu 290 Ser Ile Glu Asp 295 Pro Ser His	915
GAA GGA GAG GGA AUA CCA CUA UAU GAU GCG AUC AAG UGU AUG AGA ACA Glu Gly 300 Glu Gly Ile Pro Leu Tyr 305 Asp Ala Ile Lys Cys 310 Met Arg Thr	963
UUC UUU GGA UGG AAA GAA CCC UAU GUU GUU AAA CCA CAC GAA AAG GGA Phe Phe 315 Gly Trp Lys Glu 320 Pro Tyr Val Val Lys 325 His Glu Lys Gly	1011
AUA AAU CCA AAU UAU CUG CUG UCA UGG AAG CAA GUA CUG GCA GAA CUG Ile Asn Pro Asn Tyr 335 Leu Leu Ser Trp Lys Gln Val 340 Leu Ala Glu Leu 345	1059
CAG GAC AUU GAG AAU GAG GAG AAG AUU CCA AGA ACC AAA AAC AUG AAG Gln Asp Ile Glu Asn 350 Glu Glu Lys Ile Pro 355 Arg Thr Lys Asn Met 360 Lys	1107
AAA ACG AGU CAG CUA AAG UGG GCA CUU GGU GAG AAC AUG GCA CCA GAG Lys Thr Ser Gln 365 Leu Lys Trp Ala Leu 370 Gly Glu Asn Met 375 Ala Pro Glu	1155
AAG GUA GAC UUU GAC GAC UGU AGA GAU GUA AGC GAU UUG AAG CAA UAU Lys Val Asp Phe Asp Asp Cys 385 Arg Asp Val Ser Asp 390 Leu Lys Gln Tyr	1203
GAU AGU GAU GAA CCU GAA UUA AGG UCA CUU UCA AGC UGG AUC CAG AAU Asp Ser 395 Asp Glu Pro Glu Leu 400 Arg Ser Leu Ser 405 Trp Ile Gln Asn	1251
GAG UUC AAC AAG GCA UGC GAG CUG ACC GAU UCA AUC UGG AUA GAG CUC Glu Phe Asn Lys Ala 415 Cys Glu Leu Thr Asp Ser 420 Ile Trp Ile Glu Leu 425	1299
GAU GAG AUU GGA GAA GAU GUG GCU CCA AUU GAA CAC AUU GCA AGC AUG Asp Glu Ile Gly Glu 430 Asp Val Ala Pro Ile 435 Glu His Ile Ala 440 Ser Met	1347
AGA AGG AAU UAC UUC ACA GCA GAG GUG UCU CAU UGC AGA GCC ACA GAA Arg Arg Asn Tyr 445 Phe Thr Ala Glu Val 450 Ser His Cys Arg 455 Ala Thr Glu	1395
UAU AUA AUG AAG GGG GUA UAC AUU AAU ACU GCC UUG CUU AAU GCA UCC Tyr Ile Met Lys Gly Val Tyr Ile Asn Thr Ala Leu Leu Asn Ala Ser	1443

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460	465	470	
UGU GCA GCA AUG GAC GAU UUC CAA CUA AUU CCC AUG AUA AGC AAA UGU Cys Ala Ala Met Asp Asp Phe Gln Leu Ile Pro Met Ile Ser Lys Cys 475 480 485			1491
AGA ACU AAA GAG GGA AGG CGA AAG ACC AAU UUA UAU GGU UUC AUC AUA Arg Thr Lys Glu Gly Arg Arg Lys Thr Asn Leu Tyr Gly Phe Ile Ile 490 495 500 505			1539
AAA GGA AGA UCU CAC UUA AGG AAU GAC ACC GAC GUG GUA AAC UUU GUG Lys Gly Arg Ser His Leu Arg Asn Asp Thr Asp Val Val Asn Phe Val 510 515 520			1587
AGC AUG GAG UUU UCU CUC ACU GAC CCA AGA CUU GAG CCA CAC AAA UGG Ser Met Glu Phe Ser Leu Thr Asp Pro Arg Leu Glu Pro His Lys Trp 525 530 535			1635
GAG AAG UAC UGU GUU CUU GAG AUA GGA GAU AUG CUA CUA AGA AGU GCC Glu Lys Tyr Cys Val Leu Glu Ile Gly Asp Met Leu Leu Arg Ser Ala 540 545 550			1683
AUA GGC CAG GUG UCA AGG CCC AUG UUC UUG UAU GUG AGG ACA AAU GGA Ile Gly Gln Val Ser Arg Pro Met Phe Leu Tyr Val Arg Thr Asn Gly 555 560 565			1731
ACA UCA AAG AUU AAA AUG AAA UGG GGA AUG GAG AUG AGG CGU UGC CUC Thr Ser Lys Ile Lys Met Lys Trp Gly Met Glu Met Arg Arg Cys Leu 570 575 580 585			1779
CUU CAG UCA CUC CAA CAA AUC GAG AGU AUG AUU GAA GCC GAG UCC UCU Leu Gln Ser Leu Gln Ile Glu Ser Met Ile Glu Ala Glu Ser Ser 590 595 600			1827
GUC AAG GAG AAA GAC AUG ACC AAA GAG UUU UUC GAG AAU AAA UCA GAA Val Lys Glu Lys Asp Met Thr Lys Glu Phe Phe Glu Asn Lys Ser Glu 605 610 615			1875
ACA UGG CCC AUU GGA GAG UCC CCC AAA GGA GUG GAA GAA GGU UCC AUU Thr Trp Pro Ile Gly Glu Ser Pro Lys Gly Val Glu Glu Gly Ser Ile 620 625 630			1923
GGG AAG GUC UGC AGG ACU UUA UUA GCC AAG UCG GUA UUC AAU AGC CUG Gly Lys Val Cys Arg Thr Leu Leu Ala Lys Ser Val Phe Asn Ser Leu 635 640 645			1971
UAU GCA UCU CCA CAA UUA GAA GGA UUU UCA GCU GAA UCA AGA AAA CUG Tyr Ala Ser Pro Gln Leu Glu Gly Phe Ser Ala Glu Ser Arg Lys Leu 650 655 660 665			2019
CUU CUU GUC GUU CAG GCU CUU AGG GAC AAU CUU GAA CCU GGG ACC UUU Leu Leu Val Val Gln Ala Leu Arg Asp Asn Leu Glu Pro Gly Thr Phe 670 675 680			2067
GAU CUU GGG GGG CUA UAU GAA GCA AUU GAG GAG UGC CUG AUU AAU GAU Asp Leu Gly Gly Leu Tyr Glu Ala Ile Glu Glu Cys Leu Ile Asn Asp 685 690 695			2115
CCC UGG GUU UUG CUU AAU GCG UCU UGG UUC AAC UCC UUC CUA ACA CAU Pro Trp Val Leu Leu Asn Ala Ser Trp Phe Asn Ser Phe Leu Thr His 700 705 710			2163
GCA CCA AGA UAGUUGUGGC AAUGCUACUA UUUGCUAUCC AUACUGUCCA			2212

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Ala Pro Arg
715

AAAAAGUACC UUGUUUCUAC U

2233

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

Met Glu Asp Phe Val Arg Gln Cys Phe Asn Pro Met Ile Val Glu Leu
 1           5           10
Ala Glu Lys Ala Met Lys Glu Tyr Gly Glu Asp Leu Lys Ile Glu Thr
 20          25          30
Asn Lys Phe Ala Ala Ile Cys Thr His Leu Glu Val Cys Phe Met Tyr
 35          40          45
Ser Asp Phe His Phe Ile Asn Glu Gln Gly Glu Ser Ile Ile Val Glu
 50          55          60
Leu Asp Asp Pro Asn Ala Leu Leu Lys His Arg Phe Glu Ile Ile Glu
 65          70          75          80
Gly Arg Asp Arg Thr Met Ala Trp Thr Val Val Asn Ser Ile Cys Asn
 85          90          95
Thr Thr Gly Ala Glu Lys Pro Lys Phe Leu Pro Asp Leu Tyr Asp Tyr
100         105         110
Lys Glu Asn Arg Phe Ile Glu Ile Gly Val Thr Arg Arg Glu Val His
115         120         125
Ile Tyr Tyr Leu Glu Lys Ala Asn Lys Ile Lys Ser Glu Lys Thr His
130         135         140
Ile His Ile Phe Ser Phe Thr Gly Glu Glu Met Ala Thr Lys Ala Asp
145         150         155         160
Tyr Thr Leu Asp Glu Glu Ser Arg Ala Arg Ile Lys Thr Arg Leu Phe
165         170         175
Thr Ile Arg Gln Glu Met Ala Ser Arg Gly Leu Trp Asp Ser Phe His
180         185         190
Gln Ser Glu Arg Gly Glu Glu Thr Ile Glu Glu Arg Phe Glu Ile Thr
195         200         205
Gly Thr Met Arg Arg Leu Ala Asp Gln Ser Leu Pro Pro Asn Phe Ser
210         215         220
Cys Leu Glu Asn Phe Arg Ala Tyr Val Asp Gly Phe Glu Pro Asn Gly
225         230         235         240
Tyr Ile Glu Gly Lys Leu Ser Gln Met Ser Lys Glu Val Asn Ala Lys

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Ile	Glu	Pro	Phe 260	Leu	Lys	Thr	Thr	Pro 265	Arg	Pro	Ile	Arg	Leu 270	Pro	Asp
Gly	Pro	Pro 275	Cys	Ser	Gln	Arg	Ser 280	Lys	Phe	Leu	Leu	Met 285	Asp	Ala	Leu
Lys	Leu 290	Ser	Ile	Glu	Asp	Pro 295	Ser	His	Glu	Gly	Glu 300	Gly	Ile	Pro	Leu
Tyr 305	Asp	Ala	Ile	Lys	Cys 310	Met	Arg	Thr	Phe	Phe 315	Gly	Trp	Lys	Glu	Pro 320
Tyr	Val	Val	Lys	Pro 325	His	Glu	Lys	Gly	Ile 330	Asn	Pro	Asn	Tyr	Leu 335	Leu
Ser	Trp	Lys	Gln 340	Val	Leu	Ala	Glu	Leu 345	Gln	Asp	Ile	Glu	Asn 350	Glu	Glu
Lys	Ile	Pro 355	Arg	Thr	Lys	Asn	Met 360	Lys	Lys	Thr	Ser	Gln 365	Leu	Lys	Trp
Ala	Leu 370	Gly	Glu	Asn	Met	Ala 375	Pro	Glu	Lys	Val	Asp 380	Phe	Asp	Asp	Cys
Arg 385	Asp	Val	Ser	Asp	Leu 390	Lys	Gln	Tyr	Asp	Ser 395	Asp	Glu	Pro	Glu	Leu 400
Arg	Ser	Leu	Ser	Ser 405	Trp	Ile	Gln	Asn	Glu 410	Phe	Asn	Lys	Ala	Cys 415	Glu
Leu	Thr	Asp	Ser 420	Ile	Trp	Ile	Glu	Leu 425	Asp	Glu	Ile	Gly	Glu 430	Asp	Val
Ala	Pro	Ile 435	Glu	His	Ile	Ala	Ser 440	Met	Arg	Arg	Asn	Tyr 445	Phe	Thr	Ala
Glu	Val 450	Ser	His	Cys	Arg	Ala 455	Thr	Glu	Tyr	Ile	Met 460	Lys	Gly	Val	Tyr
Ile 465	Asn	Thr	Ala	Leu	Leu 470	Asn	Ala	Ser	Cys	Ala 475	Ala	Met	Asp	Asp	Phe 480
Gln	Leu	Ile	Pro	Met 485	Ile	Ser	Lys	Cys	Arg 490	Thr	Lys	Glu	Gly	Arg 495	Arg
Lys	Thr	Asn	Leu 500	Tyr	Gly	Phe	Ile	Ile 505	Lys	Gly	Arg	Ser	His 510	Leu	Arg
Asn	Asp	Thr 515	Asp	Val	Val	Asn	Phe 520	Val	Ser	Met	Glu	Phe 525	Ser	Leu	Thr
Asp	Pro 530	Arg	Leu	Glu	Pro	His 535	Lys	Trp	Glu	Lys	Tyr 540	Cys	Val	Leu	Glu
Ile 545	Gly	Asp	Met	Leu	Leu 550	Arg	Ser	Ala	Ile	Gly 555	Gln	Val	Ser	Arg	Pro 560
Met	Phe	Leu	Tyr	Val 565	Arg	Thr	Asn	Gly	Thr 570	Ser	Lys	Ile	Lys	Met 575	Lys
Trp	Gly	Met	Glu	Met	Arg	Arg	Cys	Leu	Leu	Gln	Ser	Leu	Gln	Gln	Ile

580		585		590
Glu Ser Met Ile Glu Ala Glu Ser Ser Val Lys Glu Lys Asp Met Thr				
595		600		605
Lys Glu Phe Phe Glu Asn Lys Ser Glu Thr Trp Pro Ile Gly Glu Ser				
610		615		620
Pro Lys Gly Val Glu Glu Gly Ser Ile Gly Lys Val Cys Arg Thr Leu				
625		630		635
Leu Ala Lys Ser Val Phe Asn Ser Leu Tyr Ala Ser Pro Gln Leu Glu				
645		650		655
Gly Phe Ser Ala Glu Ser Arg Lys Leu Leu Leu Val Val Gln Ala Leu				
660		665		670
Arg Asp Asn Leu Glu Pro Gly Thr Phe Asp Leu Gly Gly Leu Tyr Glu				
675		680		685
Ala Ile Glu Glu Cys Leu Ile Asn Asp Pro Trp Val Leu Leu Asn Ala				
690		695		700
Ser Trp Phe Asn Ser Phe Leu Thr His Ala Pro Arg				
705		710		715

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HA

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(144, "a")
- (D) OTHER INFORMATION: /gene= "HA"
/note= "u in ca "master" strain; a in wt2(3)"
/citation= ([1])

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(455, "g")
- (D) OTHER INFORMATION: /gene= "HA"
/note= "a in ca "master" strain; g in wt2(3)"
/citation= ([1])

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(729, "a")
- (D) OTHER INFORMATION: /gene= "HA"
/note= "c in ca "master" strain; a in wt2(3)"
/citation= ([1])

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(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 44..1729
 (D) OTHER INFORMATION: /product= "hemagglutinin"
 /gene= "HA"
 /note= "hemagglutinin protein"
 /citation= ([1])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
 Maassab, H F
 Webster, R G
 (B) TITLE: Molecular and biological changes in the cold
 adapted master strain A/AA/6/60 (H2N2) influenza
 virus
 (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
 (G) DATE: 1993
 (K) RELEVANT RESIDUES IN SEQ ID NO:35: FROM 1 TO 1773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGCAAAAGCA GGGGUUAUAC CAUAGACAAC CAAAAGCAAA ACA	AUG GCC AUC AUU	55
	Met Ala Ile Ile	
	1	
UAU CUC AUU CUC CUG UUC ACA GCA GUG AGA GGG GAC AAG AUA UGC AUU		103
Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Asp Lys Ile Cys Ile		
5 10 15 20		
GGA UAC CAU GCC AAU AAU UCC ACA GAG ACG GUC GAC ACA AAU CUA GAG		151
Gly Tyr His Ala Asn Asn Ser Thr Glu Thr Val Asp Thr Asn Leu Glu		
25 30 35		
CGG AAC GUC ACU GUG ACU CAU GCC AAG GAC AUU CUU GAG AAG ACC CAU		199
Arg Asn Val Thr Val Thr His Ala Lys Asp Ile Leu Glu Lys Thr His		
40 45 50		
AAC GGA AAG UUA UGC AAA CUA AAC GGA AUC CCU CCA CUU GAA CUA GGG		247
Asn Gly Lys Leu Cys Lys Leu Asn Gly Ile Pro Pro Leu Glu Leu Gly		
55 60 65		
GAC UGU AGC AUU GCC GGA UGG CUC CUU GGA AAU CCA GAA UGU GAU AGG		295
Asp Cys Ser Ile Ala Gly Trp Leu Leu Gly Asn Pro Glu Cys Asp Arg		
70 75 80		
CUU CUA AGU GUG CCA GAA UGG UCC UAU AUA AUG GAG AAA GAA AAC CCG		343
Leu Leu Ser Val Pro Glu Trp Ser Tyr Ile Met Glu Lys Glu Asn Pro		
85 90 95 100		
AGA AAC GGU UUG UGU UAU CCA GGC AAC UUC AAU GAU UAU GAA GAA UUG		391
Arg Asn Gly Leu Cys Tyr Pro Gly Asn Phe Asn Asp Tyr Glu Glu Leu		
105 110 115		
AAA CAU CUC CUC AGC AGC GUG AAA CAU UUC GAG AAA GUA AAG AUU CUG		439
Lys His Leu Leu Ser Ser Val Lys His Phe Glu Lys Val Lys Ile Leu		
120 125 130		
CCC AAA GAU AGA UGG GCA CAG CAU ACA ACA ACU GGA GGU UCA CAG GCC		487
Pro Lys Asp Arg Trp Ala Gln His Thr Thr Thr Gly Gly Ser Gln Ala		
135 140 145		

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UGC Cys 150	GCG Ala 150	GUG Val 150	UCU Ser	GGU Gly	AAU Asn	CCA Pro 155	UCA Ser	UUC Phe	UUC Phe	AGG Arg	AAC Asn 160	AUG Met	GUC Val	UGG Trp	CUG Leu	535
ACA Thr 165	GAG Glu	GAA Glu	GGA Gly	UCA Ser	AAU Asn 170	UAU Tyr	CCG Pro	GUU Val	GCC Ala	AAA Lys 175	GGA Gly	UCG Ser	UAC Tyr	AAC Asn	AAU Asn 180	583
ACA Thr	AGC Ser	GGA Gly	GAA Glu	CAA Gln 185	AUG Met	CUA Leu	AUA Ile	AUU Ile	UGG Trp 190	GGG Gly	GUG Val	CAC His	CAU His	CCC Pro 195	AUU Ile	631
GAU Asp	GAG Glu	ACA Thr	GAA Glu 200	CAA Gln	AGA Arg	ACA Thr	UUG Leu	UAC Tyr 205	CAG Gln	AAU Asn	GUG Val	GGA Gly	ACC Thr 210	UAU Tyr	GUU Val	679
UCC Ser	GUA Val 215	GGC Gly	ACA Thr	UCA Ser	ACA Thr	UUG Leu	AAC Asn 220	AAA Lys	AGG Arg	UCA Ser	ACC Thr	CCA Pro 225	GAA Glu	AUA Ile	GCA Ala	727
AAA Lys 230	AGG Arg	CCU Pro	AAA Lys	GUG Val	AAU Asn	GGA Gly 235	CUA Leu	GGA Gly	AGU Ser	AGA Arg	AUG Met 240	GAA Glu	UUC Phe	UCU Ser	UGG Trp	775
ACC Thr 245	CUC Leu	UUG Leu	GAU Asp	AUG Met	UGG Trp 250	GAC Asp	ACC Thr	AUA Ile	AAU Asn	UUU Phe 255	GAG Glu	AGU Ser	ACU Thr	GGU Gly	AAU Asn 260	823
CUA Leu	AUU Ile	GCA Ala	CCA Pro	GAG Glu 265	UAU Tyr	GGA Gly	UUC Phe	AAA Lys	AUA Ile 270	UCG Ser	AAA Lys	AGA Arg	GGU Gly	AGU Ser 275	UCU Ser	871
GGG Gly	AUC Ile	AUG Met	AAA Lys 280	ACA Thr	GAA Glu	GGA Gly	ACA Thr	CUU Leu 285	GAG Glu	AAC Asn	UGU Cys	GAG Glu	ACC Thr 290	AAA Lys	UGC Cys	919
CAA Gln	ACU Thr	CCU Pro 295	UUG Leu	GGA Gly	GCA Ala	AUA Ile	AAU Asn 300	ACA Thr	ACA Thr	UUG Leu	CCU Pro	UUU Phe 305	CAC His	AAU Asn	GUC Val	967
CAC His 310	CCA Pro	CUG Leu	ACA Thr	AUA Ile	GGU Gly	GAG Glu 315	UGC Cys	CCC Pro	AAA Lys	UAU Tyr	GUA Val 320	AAA Lys	UCG Ser	GAG Glu	AAG Lys	1015
UUG Leu 325	GUC Val	UUA Leu	GCA Ala	ACA Thr	GGA Gly 330	CUA Leu	AGG Arg	AAU Asn	GUU Val	CCC Pro 335	CAG Gln	AUU Ile	GAA Glu	UCA Ser	AGA Arg 340	1063
GGA Gly	UUG Leu	UUU Phe	GGG Gly	GCA Ala 345	AUA Ile	GCU Ala	GGU Gly	UUU Phe	AUA Ile 350	GAA Glu	GGA Gly	GGA Gly	UGG Trp	CAA Gln 355	GGA Gly	1111
AUG Met	GUU Val	GAU Asp	GGU Gly 360	UGG Trp	UAU Tyr	GGA Gly	UAC Tyr	CAU His 365	CAC His	AGC Ser	AAU Asn	GAC Asp	CAG Gln 370	GGA Gly	UCA Ser	1159
GGG Gly	UAU Tyr	GCA Ala 375	GCA Ala	GAC Asp	AAA Lys	GAA Glu	UCC Ser 380	ACU Thr	CAA Gln	AAG Lys	GCA Ala	UUU Phe 385	GAU Asp	GGA Gly	AUC Ile	1207
ACC Thr	AAC Asn 390	AAG Lys	GUA Val	AAU Asn	UCU Ser	GUG Val 395	AUU Ile	GAA Glu	AAG Lys	AUA Ile	AAC Asn 400	ACC Thr	CAA Gln	UUU Phe	GAA Glu	1255

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GCU Ala 405	GUU Val	GGG Gly	AAA Lys	GAA Glu	UUC Phe 410	AGU Ser	AAC Asn	UUA Leu	GAG Glu 415	AGA Arg	AGA Arg	CUG Leu	GAG Glu	AAC Asn	UUG Leu 420	1303
AAC Asn	AAA Lys	AAG Lys	AUG Met	GAA Glu 425	GAC Asp	GGG Gly	UUU Phe	CUA Leu	GAU Asp 430	GUG Val	UGG Trp	ACA Thr	UAC Tyr	AAU Asn 435	GCU Ala	1351
GAG Glu	CUU Leu	CUA Leu	GUU Val 440	CUG Leu	AUG Met	GAA Glu	AAU Asn	GAG Glu 445	AGG Arg	ACA Thr	CUU Leu	GAC Asp	UUU Phe 450	CAU His	GAU Asp	1399
UCU Val	AAU Lys	GUC Asn 455	AAG Leu	AAU Tyr	CUG Asp	UAU Lys	GAU Val 460	AAA Arg	GUC Met	AGA Gln	AUG Leu	CAG Arg 465	CUG Asp	AGG	GAC	1447Ser Asn
AAC Asn 470	GUC Val	AAA Lys	GAA Glu	CUA Leu	GGA Gly	AAU Asn 475	GGA Gly	UGU Cys	UUU Phe	GAA Glu	UUU Phe 480	UAU Tyr	CAC His	AAA Lys	UGU Cys	1495
GAU Asp 485	GAU Asp	GAA Glu	UGC Cys	AUG Met	AAU Asn 490	AGU Ser	GUG Val	AAA Lys	AAC Asn	GGG Gly 495	ACA Thr	UAU Tyr	GAU Asp	UAU Tyr	CCC Pro 500	1543
AAG Lys	UAU Tyr	GAA Glu	GAA Glu	GAG Glu 505	UCU Ser	AAA Lys	CUA Leu	AAU Asn	AGA Arg 510	AAU Asn	GAA Glu	AUU Ile	AAA Lys	GGG Gly 515	GUA Val	1591
AAA Lys	UUG Leu	AGC Ser	AGC Ser 520	AUG Met	GGG Gly	GUU Val	UGU Cys	CGG Arg 525	AUC Ile	CUU Leu	GCC Ala	AUU Ile	UAU Tyr 530	GCU Ala	ACA Thr	1639
GUA Val	GCA Ala	GGU Gly 535	UCU Ser	CUG Leu	UCA Ser	CUG Leu	GCA Ala 540	AUC Ile	AUG Met	AUG Met	GCU Ala	GGG Gly 545	AUC Ile	UCU Ser	UUC Phe	1687
UGG Trp 550	AUG Met	UGC Cys	UCC Ser	AAC Asn	GGG Gly 555	UCU Ser	CUG Leu	CAG Gln	UGC Cys	AGG Arg	AUC Ile 560	UGC Cys	AUA Ile			1729
UGAUUAUAAG	UCAUUUUUAUA	AUUAAAAACA	CCCUUGUUUC	UACU												1773

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Ala	Ile	Ile	Tyr	Leu	Ile	Leu	Leu	Phe	Thr	Ala	Val	Arg	Gly	Asp
1				5					10					15	
Lys	Ile	Cys	Ile	Gly	Tyr	His	Ala	Asn	Asn	Ser	Thr	Glu	Thr	Val	Asp
			20					25					30		
Thr	Asn	Leu	Glu	Arg	Asn	Val	Thr	Val	Thr	His	Ala	Lys	Asp	Ile	Leu
		35				40						45			

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Glu Lys Thr His Asn Gly Lys Leu Cys Lys Leu Asn Gly Ile Pro Pro
 50 55 60
 Leu Glu Leu Gly Asp Cys Ser Ile Ala Gly Trp Leu Leu Gly Asn Pro
 65 70 75 80
 Glu Cys Asp Arg Leu Leu Ser Val Pro Glu Trp Ser Tyr Ile Met Glu
 85 90 95
 Lys Glu Asn Pro Arg Asn Gly Leu Cys Tyr Pro Gly Asn Phe Asn Asp
 100 105 110
 Tyr Glu Glu Leu Lys His Leu Leu Ser Ser Val Lys His Phe Glu Lys
 115 120 125
 Val Lys Ile Leu Pro Lys Asp Arg Trp Ala Gln His Thr Thr Thr Gly
 130 135 140
 Gly Ser Gln Ala Cys Ala Val Ser Gly Asn Pro Ser Phe Phe Arg Asn
 145 150 155 160
 Met Val Trp Leu Thr Glu Glu Gly Ser Asn Tyr Pro Val Ala Lys Gly
 165 170 175
 Ser Tyr Asn Asn Thr Ser Gly Glu Gln Met Leu Ile Ile Trp Gly Val
 180 185 190
 His His Pro Ile Asp Glu Thr Glu Gln Arg Thr Leu Tyr Gln Asn Val
 195 200 205
 Gly Thr Tyr Val Ser Val Gly Thr Ser Thr Leu Asn Lys Arg Ser Thr
 210 215 220
 Pro Glu Ile Ala Lys Arg Pro Lys Val Asn Gly Leu Gly Ser Arg Met
 225 230 235 240
 Glu Phe Ser Trp Thr Leu Leu Asp Met Trp Asp Thr Ile Asn Phe Glu
 245 250 255
 Ser Thr Gly Asn Leu Ile Ala Pro Glu Tyr Gly Phe Lys Ile Ser Lys
 260 265 270
 Arg Gly Ser Ser Gly Ile Met Lys Thr Glu Gly Thr Leu Glu Asn Cys
 275 280 285
 Glu Thr Lys Cys Gln Thr Pro Leu Gly Ala Ile Asn Thr Thr Leu Pro
 290 295 300
 Phe His Asn Val His Pro Leu Thr Ile Gly Glu Cys Pro Lys Tyr Val
 305 310 315 320
 Lys Ser Glu Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Val Pro Gln
 325 330 335
 Ile Glu Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly
 340 345 350
 Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His Ser Asn
 355 360 365
 Asp Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala
 370 375 380

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Phe Asp Gly Ile Thr Asn Lys Val Asn Ser Val Ile Glu Lys Ile Asn
385                               390                               395                               400
Thr Gln Phe Glu Ala Val Gly Lys Glu Phe Ser Asn Leu Glu Arg Arg
                               405                               410                               415
Leu Glu Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp
                               420                               425                               430
Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu
                               435                               440                               445
Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg Met
                               450                               455                               460
Gln Leu Arg Asp Asn Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe
465                               470                               475                               480
Tyr His Lys Cys Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly Thr
                               485                               490                               495
Tyr Asp Tyr Pro Lys Tyr Glu Glu Glu Ser Lys Leu Asn Arg Asn Glu
                               500                               505                               510
Ile Lys Gly Val Lys Leu Ser Ser Met Gly Val Cys Arg Ile Leu Ala
                               515                               520                               525
Ile Tyr Ala Thr Val Ala Gly Ser Leu Ser Leu Ala Ile Met Met Ala
                               530                               535                               540
Gly Ile Ser Phe Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile
545                               550                               555                               560
cys ile

```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: NA

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(394, "c")
- (D) OTHER INFORMATION: /product= "Neuraminidase"
/gene= "NA"
/note= "u in ca "master" strain; c in wt2(3)"
/citation= ([1])

(ix) FEATURE:

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(A) NAME/KEY: mutation
(B) LOCATION: replace(604, "a")
(D) OTHER INFORMATION: /product= "Neuraminidase"
                        /gene= "NA"
                        /note= "u in ca "master" strain; a in wt2(3)"
                        /citation= ([1])
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(A) NAME/KEY: CDS
(B) LOCATION: 20..1426
(D) OTHER INFORMATION: /product= "neuraminidase"
                        /gene= "NA"
                        /note= "neuraminidase protein"
                        /citation= ([1])
```

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
(B) TITLE: Molecular and biological changes in the cold
adapted master strain A/AA/6/60 (H2N2) Influenza
Virus
(C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
(G) DATE: 1993
(K) RELEVANT RESIDUES IN SEQ ID NO:37: FROM 1 TO 1467

AGCAAAAGCA	GGAGUGAAAA	AUG Met 1	AAU Asn	CCA Pro	AAU Asn	CAA Gln 5	AAG Lys	ACA Thr	AUA Ile	ACA Thr	AUU Ile 10	GGC Gly		52		
UCU Ser	GUC Val	UCU Ser	CUC Leu 15	ACC Thr	AUC Ile	GCA Ala	ACA Thr	GUA Val 20	UGC Cys	UUC Phe	CUC Leu	AUG Met	CAG Gln 25	AUU Ile	GCC Ala	100
AUC Ile	CUG Leu	GCA Ala 30	ACU Thr	ACU Thr	GUG Val	ACA Thr	UUG Leu 35	CAC His	CUU Leu	AAG Lys	CAA Gln	CAU His 40	GAG Glu	UGC Cys	GAC Asp	148
UCC Ser	CCC Pro 45	GCG Ala	AGC Ser	AAC Asn	CAA Gln	GUA Val 50	AUG Met	CCA Pro	UGU Cys	GAA Glu	CCA Pro 55	AUA Ile	AUA Ile	AUA Ile	GAA Glu	196
AGG Arg 60	AAC Asn	AUA Ile	ACA Thr	GAG Glu	AUA Ile 65	GUG Val	UAU Tyr	UUG Leu	AAU Asn	AAC Asn 70	ACC Thr	ACC Thr	AUA Ile	GAG Glu	AAA Lys 75	244
GAG Glu	AUU Ile	UGC Cys	CCC Pro	GAA Glu 80	GUA Val	GUG Val	GGA Gly	UAC Tyr	AGA Arg 85	AAU Asn	UGG Trp	UCA Ser	AAG Lys	CCG Pro 90	CAA Gln	292
UGU Cys	CAA Gln	AUU Ile	ACA Thr 95	GGA Gly	UUU Phe	GCA Ala	CCU Pro	UUU Phe 100	UCU Ser	AAG Lys	GAC Asp	AAU Asn	UCA Ser 105	AUC Ile	CGG Arg	340
CUU Leu	UCU Ser	GCU Ala 110	GGU Gly	GGG Gly	GAC Asp	AUU Ile	UGG Trp 115	GUG Val	ACG Thr	AGA Arg	GAA Glu	CCU Pro 120	UAU Tyr	GUG Val	UCA Ser	388
UGC Cys	GAC Asp	CCU Pro	GGC Gly	AAG Lys	UGU Cys	UAU Tyr	CAA Gln	UUU Phe	GCA Ala	CUC Leu	GGG Gly	CAG Gln	GGG Gly	ACC Thr	ACA Thr	436

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125	130	135	
CUA GAC AAC AAA CAU UCA AAU GGC ACA AUA CAU GAU AGA AUC CCU CAU Leu Asp Asn Lys His Ser Asn Gly Thr Ile His Asp Arg Ile Pro His 140 145 150 155			484
CGA ACC CUA UUA AUG AAU GAG UUG GGU GUU CCA UUU CAU UUA GGA ACC Arg Thr Leu Leu Met Asn Glu Leu Gly Val Pro Phe His Leu Gly Thr 160 165 170			532
AAA CAA GUG UGU GCA GCA UGG UCC AGC UCA AGU UGU CAC GAU GGA AAA Lys Gln Val Cys Ala Ala Trp Ser Ser Ser Ser Cys His Asp Gly Lys 175 180 185			580
GCA UGG UUG CAU GUU UGU GUC ACA GGG GAU GAU AGA AAU GCA ACU GCU Ala Trp Leu His Val Cys Val Thr Gly Asp Asp Arg Asn Ala Thr Ala 190 195 200			628
AGC UUC AUU UAU GAC GGG AAG CUU GUG GAC AGU AUU GGU UCA UGG UCU Ser Phe Ile Tyr Asp Gly Lys Leu Val Asp Ser Ile Gly Ser Trp Ser 205 210 215			676
CAA AAU GUC CUC AGG ACC CAG GAG UCG GAA UGC GUC UGU AUC AAU GGG Gln Asn Val Leu Arg Thr Gln Glu Ser Glu Cys Val Cys Ile Asn Gly 220 225 230 235			724
ACU UGC ACA GUA GUA AUG ACU GAU GGA AGU GCA UCA GGA AGA GCU GAU Thr Cys Thr Val Val Met Thr Asp Gly Ser Ala Ser Gly Arg Ala Asp 240 245 250			772
ACU AGA AUA CUA UUC AUU AAA GAG GGG AAA AUU GUC CAU AUU GGC CCA Thr Arg Ile Leu Phe Ile Lys Glu Gly Lys Ile Val His Ile Gly Pro 255 260 265			820
UUG UCA GGA AGU GCU CAG CAU GUA GAG GAG UGU UCU UGU UAC CCU CGA Leu Ser Gly Ser Ala Gln His Val Glu Glu Cys Ser Cys Tyr Pro Arg 270 275 280			868
UAU CCU GAC GUC AGA UGU AUC UGC AGA GAC AAC UGG AAA GGC UCU AAU Tyr Pro Asp Val Arg Cys Ile Cys Arg Asp Asn Trp Lys Gly Ser Asn 285 290 295			916
AGG CCC GUU AUA GAC AUA AAU AUG GAA GAU UAU AGC AUU GAU UCC AGU Arg Pro Val Ile Asp Ile Asn Met Glu Asp Tyr Ser Ile Asp Ser Ser 300 305 310 315			964
UAU GUG UGC UCA GGG CUU GUU GGC GAC ACA CCC AGG AAC GAC GAC AGC Tyr Val Cys Ser Gly Leu Val Gly Asp Thr Pro Arg Asn Asp Asp Ser 320 325 330			1012
UCU AGC AAU AGC AAU UGC AGG GAU CCU AAC AAU GAG AGA GGG AAU CCA Ser Ser Asn Ser Asn Cys Arg Asp Pro Asn Asn Glu Arg Gly Asn Pro 335 340 345			1060
GGA GUG AAA GGC UGG GCC UUU GAC AAU GGA GAU GAU GUA UGG AUG GGA Gly Val Lys Gly Trp Ala Phe Asp Asn Gly Asp Asp Val Trp Met Gly 350 355 360			1108
AGA ACA AUC AGC AAA GAU UUA CGC UCA GGU UAU GAA ACU UUC AAA GUC Arg Thr Ile Ser Lys Asp Leu Arg Ser Gly Tyr Glu Thr Phe Lys Val 365 370 375			1156
AUU GGU GGU UGG UCC ACA CCU AAU UCC AAA UCG CAG GUC AAU AGA CAG			1204

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Ile 380	Gly	Gly	Trp	Ser	Thr 385	Pro	Asn	Ser	Lys	Ser 390	Gln	Val	Asn	Arg	Gln 395	
GUC	AUA	GUU	GAC	AAC	AAU	AAU	UGG	UCU	GGU	UAC	UCU	GGU	AUU	UUC	UCU	1252
Val	Ile	Val	Asp	Asn 400	Asn	Asn	Trp	Ser	Gly 405	Tyr	Ser	Gly	Ile	Phe	Ser 410	
GUU	GAG	GGC	AAA	AGC	UGC	AUC	AAU	AGG	UGC	UUU	UAU	GUG	GAG	UUG	AUA	1300
Val	Glu	Gly	Lys 415	Ser	Cys	Ile	Asn	Arg 420	Cys	Phe	Tyr	Val	Glu 425	Leu	Ile	
AGG	GGA	AGG	CCA	CAG	GAG	ACU	AGA	GUA	UGG	UGG	ACC	UCA	AAC	AGU	AUU	1348
Arg	Gly	Arg 430	Pro	Gln	Glu	Thr	Arg 435	Val	Trp	Trp	Thr	Ser 440	Asn	Ser	Ile	
GUU	GUA	UUU	UGU	GGC	ACU	UCA	GGU	ACU	UAU	GGA	ACA	GGC	UCA	UGG	CCU	1396
Val	Val	Phe	Cys	Gly	Thr	Ser 450	Gly	Thr	Tyr	Gly	Thr 455	Gly	Ser	Trp	Pro	
GAU	GGG	GCG	AAC	AUC	AAU	UUC	AUG	CCU	AUA	UAACGUUUCG	CAAUUUUAGA					1446
Asp 460	Gly	Ala	Asn	Ile 465	Asn	Phe	Met	Pro	Ile							
AAAAAACUCC	UUGUUUCUAC	U														1467

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met 1	Asn	Pro	Asn	Gln 5	Lys	Thr	Ile	Thr	Ile 10	Gly	Ser	Val	Ser	Leu	Thr 15
Ile	Ala	Thr	Val 20	Cys	Phe	Leu	Met	Gln 25	Ile	Ala	Ile	Leu	Ala	Thr	Thr 30
Val	Thr	Leu 35	His	Leu	Lys	Gln 40	His	Glu	Cys	Asp	Ser	Pro	Ala	Ser	Asn 45
Gln	Val 50	Met	Pro	Cys	Glu	Pro 55	Ile	Ile	Ile	Glu	Arg 60	Asn	Ile	Thr	Glu 65
Ile 65	Val	Tyr	Leu	Asn 70	Asn	Thr	Thr	Ile	Glu	Lys 75	Glu	Ile	Cys	Pro	Glu 80
Val	Val	Gly	Tyr 85	Arg	Asn	Trp	Ser	Lys	Pro 90	Gln	Cys	Gln	Ile	Thr	Gly 95
Phe	Ala	Pro	Phe 100	Ser	Lys	Asp	Asn	Ser 105	Ile	Arg	Leu	Ser	Ala	Gly	Gly 110
Asp	Ile	Trp 115	Val	Thr	Arg	Glu	Pro 120	Tyr	Val	Ser	Cys	Asp 125	Pro	Gly	Lys 130
Cys	Tyr 130	Gln	Phe	Ala	Leu	Gly 135	Gln	Gly	Thr	Thr	Leu 140	Asp	Asn	Lys	His 145

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Ser Asn Gly Thr Ile His Asp Arg Ile Pro His Arg Thr Leu Leu Met
 145 150 155 160
 Asn Glu Leu Gly Val Pro Phe His Leu Gly Thr Lys Gln Val Cys Ala
 165 170 175
 Ala Trp Ser Ser Ser Cys His Asp Gly Lys Ala Trp Leu His Val
 180 185 190
 Cys Val Thr Gly Asp Asp Arg Asn Ala Thr Ala Ser Phe Ile Tyr Asp
 195 200 205
 Gly Lys Leu Val Asp Ser Ile Gly Ser Trp Ser Gln Asn Val Leu Arg
 210 215 220
 Thr Gln Glu Ser Glu Cys Val Cys Ile Asn Gly Thr Cys Thr Val Val
 225 230 235 240
 Met Thr Asp Gly Ser Ala Ser Gly Arg Ala Asp Thr Arg Ile Leu Phe
 245 250 255
 Ile Lys Glu Gly Lys Ile Val His Ile Gly Pro Leu Ser Gly Ser Ala
 260 265 270
 Gln His Val Glu Glu Cys Ser Cys Tyr Pro Arg Tyr Pro Asp Val Arg
 275 280 285
 Cys Ile Cys Arg Asp Asn Trp Lys Gly Ser Asn Arg Pro Val Ile Asp
 290 295 300
 Ile Asn Met Glu Asp Tyr Ser Ile Asp Ser Ser Tyr Val Cys Ser Gly
 305 310 315 320
 Leu Val Gly Asp Thr Pro Arg Asn Asp Asp Ser Ser Ser Asn Ser Asn
 325 330 335
 Cys Arg Asp Pro Asn Asn Glu Arg Gly Asn Pro Gly Val Lys Gly Trp
 340 345 350
 Ala Phe Asp Asn Gly Asp Asp Val Trp Met Gly Arg Thr Ile Ser Lys
 355 360 365
 Asp Leu Arg Ser Gly Tyr Glu Thr Phe Lys Val Ile Gly Gly Trp Ser
 370 375 380
 Thr Pro Asn Ser Lys Ser Gln Val Asn Arg Gln Val Ile Val Asp Asn
 385 390 395 400
 Asn Asn Trp Ser Gly Tyr Ser Gly Ile Phe Ser Val Glu Gly Lys Ser
 405 410 415
 Cys Ile Asn Arg Cys Phe Tyr Val Glu Leu Ile Arg Gly Arg Pro Gln
 420 425 430
 Glu Thr Arg Val Trp Trp Thr Ser Asn Ser Ile Val Val Phe Cys Gly
 435 440 445
 Thr Ser Gly Thr Tyr Gly Thr Gly Ser Trp Pro Asp Gly Ala Asn Ile
 450 455 460
 Asn Phe Met Pro Ile
 465

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(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: NP

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(113, "a")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain; a in wt2(3); c in 1988 reported wild type E28-32 strain (manuscript) but a in 1988 reported wild type E28-32 strain /citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(146, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain" /citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(627, "c")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain" /citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(909, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); c in 1988 reported wild type E28-32 strain" /citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1550, "a")
- (D) OTHER INFORMATION: /note= "a in ca "master" strain and in wt2(3); deletion in 1988 reported wild type E28-32 strain" /citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 46..1539
- (D) OTHER INFORMATION: /product= "Nucleoprotein" /gene= "NP" /note= "nucleoprotein" /citation= ([1][2])

(x) PUBLICATION INFORMATION:

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- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R W
- (B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
- (G) DATE: 1993
- (K) RELEVANT RESIDUES IN SEQ ID NO:39: FROM 1 TO 1566
- (x) PUBLICATION INFORMATION:
- (A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C
- (B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain, A/Ann Arbor/6/60 (H2N2)
- (C) JOURNAL: Virology
- (D) VOLUME: 167
- (F) PAGES: 554-567
- (G) DATE: 1988
- (K) RELEVANT RESIDUES IN SEQ ID NO:39: FROM 1 TO 1566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGCAAAAGCA GGGUAGAUAA UCACUCACUG AGUGACAUCA AAAUC AUG GCG UCC	54
Met Ala Ser	
1	
CAA GGC ACC AAA CGG UCU UAU GAA CAG AUG GAA ACU GAU GGG GAA CGC	102
Gln Gly Thr Lys Arg Ser Tyr Glu Gln Met Glu Thr Asp Gly Glu Arg	
5 10 15	
CAG AAU GCA AAU GAA AUC AGA GCA UCC GUC GGG AAG AUG AUU GGU GGA	150
Gln Asn Ala Asn Glu Ile Arg Ala Ser Val Gly Lys Met Ile Gly Gly	
20 25 30 35	
AUU GGA CGA UUC UAC AUC CAA AUG UGC ACC GAA CUU AAA CUC AGU GAU	198
Ile Gly Arg Phe Tyr Ile Gln Met Cys Thr Glu Leu Lys Leu Ser Asp	
40 45 50	
UAU GAG GGG CGG CUG AUC CAG AAC AGC UUA ACA AUA GAG AGA AUG GUG	246
Tyr Glu Gly Arg Leu Ile Gln Asn Ser Leu Thr Ile Glu Arg Met Val	
55 60 65	
CUC UCU GCU UUU GAC GAG AGG AGG AAU AAA UAU CUG GAA GAA CAU CCC	294
Leu Ser Ala Phe Asp Glu Arg Arg Asn Lys Tyr Leu Glu Glu His Pro	
70 75 80	
AGC GCG GGG AAG GAU CCU AAG AAA ACU GGA GGA CCC AUA UAC AAG AGA	342
Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Gly Pro Ile Tyr Lys Arg	
85 90 95	
GUA GAU GGA AAG UGG AUG AGG GAA CUC GUC CUU UAU GAC AAA GAA GAA	390
Val Asp Gly Lys Trp Met Arg Glu Leu Val Leu Tyr Asp Lys Glu Glu	
100 105 110 115	
AUA AGG CGA AUC UGG CGC CAA GCU AAU AAU GGU GAU GAU GCA ACA GCU	438
Ile Arg Arg Ile Trp Arg Gln Ala Asn Asn Gly Asp Asp Ala Thr Ala	
120 125 130	

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GGU CUG ACU CAC AUG AUG AUC UGG CAU UCC AAU UUG AAU GAU ACA ACA Gly Leu Thr His 135 Met Met Ile Trp His 140 Ser Asn Leu Asn 145 Asp Thr Thr	486
UAC CAG AGG ACA AGA GCU CUU GUU CGC ACC GGA AUG GAU CCC AGG AUG Tyr Gln Arg Thr Arg Ala Leu Val 155 Arg Thr Gly Met 160 Asp Pro Arg Met	534
UGC UCU UUG AUG CAG GGU UCG ACU CUC CCU AGG AGG UCU GGA GCC GCA Cys Ser 165 Leu Met Gln Gly Ser 170 Thr Leu Pro Arg Arg 175 Ser Gly Ala Ala	582
GGC GCU GCA GUC AAA GGA GUU GGG ACA AUG GUG AUG GAG UUG AUC AGG Gly Ala Ala Val Lys 185 Gly Val Gly Thr Met 190 Val Met Glu Leu Ile Arg 195	630
AUG AUC AAA CGU GGG AUC AAU GAU CGG AAC UUC UGG AGA GGU GAG AAU Met Ile Lys Arg 200 Gly Ile Asn Asp Arg Asn 205 Phe Trp Arg Gly 210 Glu Asn	678
GGG CGG AAA ACA AGG AAU GCU UAU GAG AGA AUG UGC AAC AUU CUC AAA Gly Arg Lys Thr 215 Arg Asn Ala Tyr Glu Arg Met Cys Asn 225 Ile Leu Lys	726
GGA AAA UUU CAA ACA GCU GCA CAA AGA GCA AUG AUG GAU CAA GUG AGA Gly Lys 230 Phe Gln Thr Ala Ala Gln 235 Arg Ala Met Met 240 Asp Gln Val Arg	774
GAA AGC CGG AAC CCA GGA AAU GCU GAG AUC GAA GAU CUC AUC UUU CUG Glu Ser 245 Arg Asn Pro Gly Asn 250 Ala Glu Ile Glu 255 Asp Leu Ile Phe Leu	822
GCA CGG UCU GCA CUC AUA UUG AGA GGG UCA GUU GCU CAC AAA UCU UGU Ala Arg Ser Ala Leu Ile 265 Leu Arg Gly Ser 270 Val Ala His Lys Ser Cys 275	870
CUG CCU GCC UGU GUG UAU GGA CCU GCC GUA GCC AGU GGG UAC GAC UUC Leu Pro Ala Cys Val 280 Tyr Gly Pro Ala Val 285 Ala Ser Gly Tyr Asp 290 Phe	918
GAA AAA GAG GGA UAC UCU UUA GUA GGG AUA GAC CCU UUC AAA CUG CUU Glu Lys 295 Glu Gly Tyr Ser Leu Val Gly 300 Ile Asp Pro Phe 305 Lys Leu Leu	966
CAA AAC AGC CAA GUA UAC AGC CUA AUC AGA CCG AAU GAG AAU CCA GCA Gln Asn 310 Ser Gln Val Tyr Ser Leu 315 Ile Arg Pro Asn 320 Glu Asn Pro Ala	1014
CAC AAG AGU CAG CUG GUG UGG AUG GCA UGC AAU UCU GCU GCA UUU GAA His Lys 325 Ser Gln Leu Val Trp 330 Met Ala Cys Asn 335 Ser Ala Ala Phe Glu	1062
GAU CUA AGA GUA UCA AGC UUC AUC AGA GGG ACC AAA GUA AUC CCA AGG Asp Leu Arg Val Ser 345 Phe Ile Arg Gly Thr 350 Lys Val Ile Pro Arg 355	1110
GGG AAA CUU UCC ACU AGA GGA GUA CAA AUU GCU UCA AAU GAA AAC AUG Gly Lys Leu Ser Thr 360 Arg Gly Val Gln 365 Ile Ala Ser Asn 370 Glu Asn Met	1158
GAU ACU AUG GGA UCA AGU ACU CUU GAA CUG AGA AGC AGG UAC UGG GCC Asp Thr Met Gly Ser Ser Thr Leu Glu Leu Arg Ser Arg Tyr Trp Ala	1206

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375	380	385	
AUA AGG ACC AGA AGU GGA GGA AAC ACU AAU CAA CAG AGG GCC UCU GCA Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg Ala Ser Ala 390 395 400			1254
GGU CAA AUC AGU GUA CAA CCU ACG UUU UCU GUG CAA AGA AAC CUC CCA Gly Gln Ile Ser Val Gln Pro Thr Phe Ser Val Gln Arg Asn Leu Pro 405 410 415			1302
UUU GAC AAA CCA ACC AUC AUG GCA GCA UUC ACU GGG AAU GCA GAG GGA Phe Asp Lys Pro Thr Ile Met Ala Ala Phe Thr Gly Asn Ala Glu Gly 420 425 430 435			1350
AGA ACA UCA GAC AUG AGG GCA GAA AUC AUA AGG AUG AUG GAA GGU GCA Arg Thr Ser Asp Met Arg Ala Glu Ile Ile Arg Met Met Glu Gly Ala 440 445 450			1398
AAA CCA GAA GAA GUG UCC UUC CAG GGG CGG GGA GUC UUC GAG CUC UCG Lys Pro Glu Glu Val Ser Phe Gln Gly Arg Gly Val Phe Glu Leu Ser 455 460 465			1446
GAC GAA AAG GCA ACG AAC CCG AUC GUG CCC UCU UUU GAC AUG AGU AAU Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp Met Ser Asn 470 475 480			1494
GAA GGA UCU UAU UUC UUC GGA GAC AAU GCA GAG GAG UAC GAC AAU Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr Asp Asn 485 490 495			1539
UAAGGAAAAA AUACCCUUGU UUCUACU			1566

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 498 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met	Ala	Ser	Gln	Gly	Thr	Lys	Arg	Ser	Tyr	Glu	Gln	Met	Glu	Thr	Asp
1				5					10					15	
Gly	Glu	Arg	Gln	Asn	Ala	Asn	Glu	Ile	Arg	Ala	Ser	Val	Gly	Lys	Met
			20					25					30		
Ile	Gly	Gly	Ile	Gly	Arg	Phe	Tyr	Ile	Gln	Met	Cys	Thr	Glu	Leu	Lys
			35				40					45			
Leu	Ser	Asp	Tyr	Glu	Gly	Arg	Leu	Ile	Gln	Asn	Ser	Leu	Thr	Ile	Glu
			50			55				60					
Arg	Met	Val	Leu	Ser	Ala	Phe	Asp	Glu	Arg	Arg	Asn	Lys	Tyr	Leu	Glu
					70				75					80	
Glu	His	Pro	Ser	Ala	Gly	Lys	Asp	Pro	Lys	Lys	Thr	Gly	Gly	Pro	Ile
				85				90						95	
Tyr	Lys	Arg	Val	Asp	Gly	Lys	Trp	Met	Arg	Glu	Leu	Val	Leu	Tyr	Asp

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100	105	110
Lys Glu Glu Ile Arg Arg Ile Trp Arg Gln Ala Asn Asn Gly Asp Asp	115	120 125
Ala Thr Ala Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn	130	135 140
Asp Thr Thr Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp	145	150 155 160
Pro Arg Met Cys Ser Leu Met Gln Gly Ser Thr Leu Pro Arg Arg Ser	165	170 175
Gly Ala Ala Gly Ala Ala Val Lys Gly Val Gly Thr Met Val Met Glu	180	185 190
Leu Ile Arg Met Ile Lys Arg Gly Ile Asn Asp Arg Asn Phe Trp Arg	195	200 205
Gly Glu Asn Gly Arg Lys Thr Arg Asn Ala Tyr Glu Arg Met Cys Asn	210	215 220
Ile Leu Lys Gly Lys Phe Gln Thr Ala Ala Gln Arg Ala Met Met Asp	225	230 235 240
Gln Val Arg Glu Ser Arg Asn Pro Gly Asn Ala Glu Ile Glu Asp Leu	245	250 255
Ile Phe Leu Ala Arg Ser Ala Leu Ile Leu Arg Gly Ser Val Ala His	260	265 270
Lys Ser Cys Leu Pro Ala Cys Val Tyr Gly Pro Ala Val Ala Ser Gly	275	280 285
Tyr Asp Phe Glu Lys Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe	290	295 300
Lys Leu Leu Gln Asn Ser Gln Val Tyr Ser Leu Ile Arg Pro Asn Glu	305	310 315 320
Asn Pro Ala His Lys Ser Gln Leu Val Trp Met Ala Cys Asn Ser Ala	325	330 335
Ala Phe Glu Asp Leu Arg Val Ser Ser Phe Ile Arg Gly Thr Lys Val	340	345 350
Ile Pro Arg Gly Lys Leu Ser Thr Arg Gly Val Gln Ile Ala Ser Asn	355	360 365
Glu Asn Met Asp Thr Met Gly Ser Ser Thr Leu Glu Leu Arg Ser Arg	370	375 380
Tyr Trp Ala Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg	385	390 395 400
Ala Ser Ala Gly Gln Ile Ser Val Gln Pro Thr Phe Ser Val Gln Arg	405	410 415
Asn Leu Pro Phe Asp Lys Pro Thr Ile Met Ala Ala Phe Thr Gly Asn	420	425 430
Ala Glu Gly Arg Thr Ser Asp Met Arg Ala Glu Ile Ile Arg Met Met		

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435

440

445

Glu Gly Ala Lys Pro Glu Glu Val Ser Phe Gln Gly Arg Gly Val Phe
450 455 460

Glu Leu Ser Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp
465 470 475 480

Met Ser Asn Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr
485 490 495

Asp Asn